OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 07:33:45 ; Search time 1640.18 Seconds
(without alignments)
108.616 Million cell updates/sec

Title: US-09-540-843-9
Perfect score: 11
Sequence: 1 ctaaccctaac 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 60474

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	11	100.0	19	17	AZ614760	AZ614760 1M0443A17
	2	11	100.0	20	17	TA158A03P	AL472050 T. brucei
c	3	11	100.0	25	17	TA84A06P	AL462065 T. brucei
	4	11	100.0	27	17	AZ803795	AZ803795 2M0064D22
	5	11	100.0	40	17	AZ380089	AZ380089 1M0135K14
c	6	9.4	85.5	22	17	AZ666649	AZ666649 1M0548M19
	7	9.4	85.5	29	17	AZ514597	AZ514597 1M0361E14
c	8	9.4	85.5	33	12	BG419809	BG419809 602453261
	9	9.4	85.5	33	17	AZ334282	AZ334282 1M0063B08
	10	9.4	85.5	34	17	AZ776073	AZ776073 2M0009M20
	11	9.4	85.5	36	17	AL767851	AL767851 Arabidops
c	12	9.4	85.5	39	9	AU008671	AU008671 AU008671
	13	9	81.8	22	14	D18745	D18745 MUSGS01807
c	14	9	81.8	31	17	AL756692	AL756692 Arabidops
	15	9	81.8	32	9	AU255689	AU255689 AU255689
	16	9	81.8	33	17	BH862417	BH862417 SALK_0898
	17	9	81.8	34	17	AZ643251	AZ643251 1M0506F04
c	18	9	81.8	36	17	BH789800	BH789800 SALK_0467
	19	9	81.8	40	9	AI507758	AI507758 sb12c12.y
	20	9	81.8	40	14	W12126	W12126 ma60g05.r1
c	21	8.4	76.4	21	17	AZ766315	AZ766315 1M0563K14
	22	8.4	76.4	23	17	TA319C11P	AL492458 T. brucei
	23	8.4	76.4	24	9	AU256889	AU256889 AU256889
c	24	8.4	76.4	25	10	AV544203	AV544203 AV544203
	25	8.4	76.4	25	17	TA274G11Q	AL485967 T. brucei
	26	8.4	76.4	27	9	AU255344	AU255344 AU255344
	27	8.4	76.4	27	14	L32043	L32043 HUMXP2G6A H
c	28	8.4	76.4	27	17	AZ789654	AZ789654 2M0037G08
c	29	8.4	76.4	30	10	BE385567	BE385567 601275826
	30	8.4	76.4	30	17	AZ761166	AZ761166 1M0555A21
c	31	8.4	76.4	31	10	BE409249	BE409249 601301117
	32	8.4	76.4	31	13	BM017239	BM017239 603643882
	33	8.4	76.4	31	17	AZ782241	AZ782241 2M0022A21
c	34	8.4	76.4	32	12	BE901763	BE901763 601675392
	35	8.4	76.4	32	17	AZ803815	AZ803815 2M0064H19
	36	8.4	76.4	32	17	AL766020	AL766020 Arabidops
	37	8.4	76.4	33	17	AZ591773	AZ591773 1M0402M06
c	38	8.4	76.4	34	9	AI047833	AI047833 ud64c05.x
c	39	8.4	76.4	34	9	AI132658	AI132658 ue33b11.x
c	40	8.4	76.4	34	12	BE729288	BE729288 601561653
	41	8.4	76.4	34	13	BI913027	BI913027 603176563
	42	8.4	76.4	34	17	TA293C07Q	AL485635 T. brucei
	43	8.4	76.4	35	9	AU263853	AU263853 AU263853
	44	8.4	76.4	35	17	AZ389531	AZ389531 1M0150P07
	45	8.4	76.4	36	14	R77023	R77023 yi66d09.r1

ALIGNMENTS

RESULT 1
AZ614760/c
LOCUS AZ614760 19 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0443A17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0443A17 R, DNA sequence.
ACCESSION AZ614760
VERSION AZ614760.1 GI:11736950
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0443 row: A column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

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FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0443A17"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        3 a      0 c      10 g      6 t
ORIGIN
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  Query Match             100.0%;  Score 11;  DB 17;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              |||||||||||
Db         19 CTAACCCTAAC 9
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```
RESULT 2
TA158A03P
LOCUS       TA158A03P                 20 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 158a03, forward sequence,
            genomic survey sequence.
ACCESSION   AL472050
VERSION     AL472050.1  GI:11837404
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Trypanosoma brucei"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="158a03"
BASE COUNT        6 a      11 c      0 g      3 t
ORIGIN
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  Query Match             100.0%;  Score 11;  DB 17;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7.2e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              |||||||||||
Db          4 CTAACCCTAAC 14
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```
RESULT 3
TA84A06P/c
LOCUS       TA84A06P                  25 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 84a06, forward sequence,
            genomic survey sequence.
ACCESSION   AL462065
VERSION     AL462065.1  GI:11860923
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Trypanosoma brucei"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="84a06"
BASE COUNT        4 a      0 c      12 g      9 t
ORIGIN
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  Query Match             100.0%;  Score 11;  DB 17;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 7.8e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              |||||||||||
Db         22 CTAACCCTAAC 12
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RESULT 4
AZ803795
LOCUS       AZ803795                 27 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0064D22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0064D22 F, DNA sequence.
ACCESSION   AZ803795
VERSION     AZ803795.1  GI:12956118
KEYWORDS    GSS..
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0064  row: D  column: 22
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 27.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0064D22"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        9 a     11 c      2 g      5 t
ORIGIN

  Query Match           100.0%;  Score 11;  DB 17;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 7.9e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||
Db         10 CTAACCCTAAC 20
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RESULT 5
AZ380089
LOCUS       AZ380089                 40 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0135K14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0135K14 R, DNA sequence.
ACCESSION   AZ380089
VERSION     AZ380089.1  GI:10493789
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0135  row: K  column: 14
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 40.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0135K14"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       14 a     15 c      1 g     10 t
ORIGIN

  Query Match           100.0%;  Score 11;  DB 17;  Length 40;
  Best Local Similarity  100.0%;  Pred. No. 8.9e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||
Db          2 CTAACCCTAAC 12
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RESULT 6
AZ666649/c
LOCUS       AZ666649                 22 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0548M19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0548M19 R, DNA sequence.
ACCESSION   AZ666649
VERSION     AZ666649.1  GI:11803795
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0548  row: M  column: 19
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0548M19"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        3 a      0 c     14 g      5 t
ORIGIN

  Query Match             85.5%;  Score 9.4;  DB 17;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 6.9e+04;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||| |||||||
Db         14 CTACCCCTAAC 4
```

```
RESULT 7
AZ514597
LOCUS       AZ514597                 29 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0361E14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0361E14 F, DNA sequence.
ACCESSION   AZ514597
VERSION     AZ514597.1  GI:10695829
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0361  row: E  column: 14
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 29.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0361E14"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        6 a      9 c      6 g      8 t
ORIGIN

  Query Match             85.5%;  Score 9.4;  DB 17;  Length 29;
  Best Local Similarity   90.9%;  Pred. No. 7.5e+04;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              |||||||| ||
Db          2 CTAACCCTTAC 12
```

```
RESULT 8
BG419809/c
LOCUS       BG419809                 33 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602453261F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4591599 5',
            mRNA sequence.
ACCESSION   BG419809
VERSION     BG419809.1  GI:13326315
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1328  row: j  column: 16
            High quality sequence stop: 33.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4591599"
                     /clone_lib="NIH_MGC_14"
                     /tissue_type="renal cell adenocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT        9 a      3 c     12 g      9 t
ORIGIN

  Query Match             85.5%;  Score 9.4;  DB 12;  Length 33;
  Best Local Similarity   90.9%;  Pred. No. 7.8e+04;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              || ||||||||
Db         17 CTCACCCTAAC 7


RESULT 9
AZ334282
LOCUS       AZ334282                 33 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0063B08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0063B08 R, DNA sequence.
ACCESSION   AZ334282
VERSION     AZ334282.1  GI:10401456
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0063  row: B  column: 08
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 33.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0063B08"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       11 a     13 c      2 g      7 t
ORIGIN

  Query Match             85.5%;  Score 9.4;  DB 17;  Length 33;
  Best Local Similarity   90.9%;  Pred. No. 7.8e+04;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||| |||
Db         12 CTAACCCCAAC 22


RESULT 10
AZ776073
LOCUS       AZ776073                 34 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0009M20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0009M20 F, DNA sequence.
ACCESSION   AZ776073
VERSION     AZ776073.1  GI:12903271
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
```

```
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0009  row: M  column: 20
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 34.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0009M20"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       19 a      9 c      2 g      4 t
ORIGIN

  Query Match             85.5%;  Score 9.4;  DB 17;  Length 34;
  Best Local Similarity   90.9%;  Pred. No. 7.9e+04;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||| |||||
Db         10 CTAACTCTAAC 20


RESULT 11
AL767851
LOCUS       AL767851                 36 bp    DNA     linear   GSS 18-JUN-2002
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-222E01-014236,
            genomic survey sequence.
ACCESSION   AL767851
VERSION     AL767851.1  GI:21520970
KEYWORDS    GSS.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE     A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 36)
  AUTHORS   Rosso,M., Strizhov,N., Li,Y. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion within the locus defined by clone F28H19.
            The sequences are generated at the MPI for Plant Breeding Research
            in the context of the GABI-Kat project. GABI-Kat is part of the
            German Plant Genomics program designated 'GABI'. Information on
            line availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-222E01-014236"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161. The lines contain one or more T-DNA
                     insertions. The DNA fragment(s) resulting from the PCR
                     were directly sequenced to determine the genomic sequence
                     flanking the insertion. Sequences displaying significant
                     similarity to the A. thalaina nuclear genome sequence were
                     processed for submission. T-DNA derived sequences were
                     removed"
BASE COUNT       14 a     10 c      4 g      8 t
ORIGIN

  Query Match             85.5%;  Score 9.4;  DB 17;  Length 36;
  Best Local Similarity   90.9%;  Pred. No. 8e+04;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||| |
Db         14 CTAACCCTATC 24


RESULT 12
AU008671/c
LOCUS       AU008671                 39 bp    mRNA    linear   EST 31-JUL-1998
DEFINITION  AU008671 Schizosaccharomyces pombe late log phase cDNA
            Schizosaccharomyces pombe cDNA clone spc03845, mRNA sequence.
ACCESSION   AU008671
VERSION     AU008671.1  GI:3345129
KEYWORDS    EST.
SOURCE      fission yeast.
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
            Schizosaccharomycetales; Schizosaccharomycetaceae;
            Schizosaccharomyces.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Morimyo,M. and Mita,K.
  TITLE     Identification of expressed sequence tags of Schizosaccharomyces
            pombe
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Mitsuoki Morimyo
            Genome Research Group
            National Institute of Radiological Sciences
            9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
            Email: morimyo@nirs.go.jp.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Schizosaccharomyces pombe"
```

/strain="972"
/db_xref="taxon:4896"
/clone="spc03845"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"
/note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"
BASE COUNT 11 a 3 c 12 g 13 t
ORIGIN

Query Match 85.5%; Score 9.4; DB 9; Length 39;
Best Local Similarity 90.9%; Pred. No. 8.2e+04;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTAACCCTAAC 11
||||||||| |
Db 34 CTAACCCTAGC 24

RESULT 13
D18745
LOCUS D18745 22 bp mRNA linear EST 12-DEC-1995
DEFINITION MUSGS01807 Mouse 3'-directed Mus musculus domesticus cDNA clone md1403 3', mRNA sequence.
ACCESSION D18745
VERSION D18745.1 GI:1100714
KEYWORDS EST.
SOURCE western European house mouse.
ORGANISM Mus musculus domesticus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara,K.
TITLE Analysis of gene expression in mouse embryogenesis by 3'-directed cDNA sequencing
JOURNAL Unpublished (1995)
COMMENT Contact: Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara,K.
Institute for Cellular and Molecular Biology
Osaka University
3-1 Yamada-oka, Suita, Osaka 565, Japan.
FEATURES Location/Qualifiers
source 1. .22
/organism="Mus musculus domesticus"
/strain="C57BL/6J"
/db_xref="taxon:10092"
/clone="md1403"
/clone_lib="Mouse 3'-directed"
/tissue_type="decidual tissue (day 6.5-8.5 of gestation)"
BASE COUNT 7 a 5 c 1 g 9 t
ORIGIN

Query Match 81.8%; Score 9; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TAACCCTAA 10
|||||||||
Db 13 TAACCCTAA 21

RESULT 14
AL756692/c
LOCUS AL756692 31 bp DNA linear GSS 17-JUN-2002
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-111H11-012331, genomic survey sequence.
ACCESSION AL756692
VERSION AL756692.1 GI:21489190
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H. and Weisshaar,B.
TITLE A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
JOURNAL Unpublished
REFERENCE 2
AUTHORS Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
TITLE A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 31)
AUTHORS Strizhov,N., Rosso,M., Li,Y. and Weisshaar,B.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence is recovered from the right border of the T-DNA. It indicates an insertion close to or within gene At1g17190. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES Location/Qualifiers
source 1. .31
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-111H11-012331"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"
BASE COUNT 8 a 0 c 10 g 13 t
ORIGIN

Query Match 81.8%; Score 9; DB 17; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AACCCTAAC 11
|||||||||
Db 18 AACCCTAAC 10

RESULT 15
AU255689
LOCUS AU255689 32 bp mRNA linear EST 25-APR-2002
DEFINITION AU255689 3'-directed mouse cDNA library Mus musculus cDNA clone BED0006171 3', mRNA sequence.
ACCESSION AU255689
VERSION AU255689.1 GI:20318670
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 32)
AUTHORS Kato,K. and Matoba,R.
TITLE Generation of expressed sequence tags from mouse brain
JOURNAL Unpublished (2002)

```
COMMENT     Contact: Kikuya Kato
            Graduate School of Biological Sciences
            Nara Institute of Science and Technology
            8916-5 Takayama, Ikoma, Nara 630-0101, Japan
            Tel: 81-743-72-5581
            Fax: 81-743-72-5589
            Email: kkato@bs.aist-nara.ac.jp,
            URL:http://love2.aist-nara.ac.jp/BED/index.html.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="BED0006171"
                     /clone_lib="3'-directed mouse cDNA library"
                     /tissue_type="brain"
                     /note="Vector: pGEM-T-easy"
BASE COUNT       10 a      8 c      6 g      8 t
ORIGIN

  Query Match             81.8%;  Score 9;  DB 9;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TAACCCTAA 10
              |||||||||
Db         23 TAACCCTAA 31


Search completed: July  6, 2003, 09:39:47
Job time : 1645.18 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 06:42:31 ; Search time 522.5 Seconds
(without alignments)
612.691 Million cell updates/sec

Title: US-09-540-843-9
Perfect score: 11
Sequence: 1 ctaaccctaac 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 774614

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		11	100.0	11	6	AR016034	AR016034 Sequence
2	c	11	100.0	11	6	AR026486	AR026486 Sequence
3		11	100.0	11	6	AR026487	AR026487 Sequence
4		11	100.0	11	6	AR059195	AR059195 Sequence
5		11	100.0	11	6	AR075506	AR075506 Sequence
6		11	100.0	11	6	AR161904	AR161904 Sequence
7		11	100.0	11	6	AX033373	AX033373 Sequence
8	c	11	100.0	11	6	AX268757	AX268757 Sequence
9		11	100.0	11	6	AX268761	AX268761 Sequence
10	c	11	100.0	11	6	AX283296	AX283296 Sequence
11		11	100.0	11	6	I31749	I31749 Sequence 2
12		11	100.0	15	6	AR026479	AR026479 Sequence
13		11	100.0	16	6	AR050942	AR050942 Sequence
14		11	100.0	16	6	AR204610	AR204610 Sequence
15		11	100.0	16	6	I51743	I51743 Sequence 11
16	c	11	100.0	17	6	A84605	A84605 Sequence 15
17	c	11	100.0	17	6	AR026488	AR026488 Sequence
18		11	100.0	17	6	AR145675	AR145675 Sequence
19		11	100.0	17	6	AR145676	AR145676 Sequence
20	c	11	100.0	18	6	A79654	A79654 Sequence 3
21		11	100.0	18	6	A79665	A79665 Sequence 14
22	c	11	100.0	18	6	A84598	A84598 Sequence 8
23		11	100.0	18	6	A84599	A84599 Sequence 9
24	c	11	100.0	18	6	AR016059	AR016059 Sequence
25	c	11	100.0	18	6	AR026482	AR026482 Sequence
26	c	11	100.0	18	6	AR026483	AR026483 Sequence
27		11	100.0	18	6	AR026484	AR026484 Sequence
28	c	11	100.0	18	6	AR037860	AR037860 Sequence
29	c	11	100.0	18	6	AR037861	AR037861 Sequence
30		11	100.0	18	6	AR037862	AR037862 Sequence
31	c	11	100.0	18	6	AR050936	AR050936 Sequence
32	c	11	100.0	18	6	AR050962	AR050962 Sequence
33	c	11	100.0	18	6	AR053263	AR053263 Sequence
34	c	11	100.0	18	6	AR054739	AR054739 Sequence
35	c	11	100.0	18	6	AR054740	AR054740 Sequence
36		11	100.0	18	6	AR054741	AR054741 Sequence
37		11	100.0	18	6	AR059509	AR059509 Sequence
38		11	100.0	18	6	AR059546	AR059546 Sequence
39	c	11	100.0	18	6	AR059547	AR059547 Sequence
40	c	11	100.0	18	6	AR069393	AR069393 Sequence
41	c	11	100.0	18	6	AR069394	AR069394 Sequence
42		11	100.0	18	6	AR069395	AR069395 Sequence
43	c	11	100.0	18	6	AR075504	AR075504 Sequence
44	c	11	100.0	18	6	AR079895	AR079895 Sequence
45		11	100.0	18	6	AR079896	AR079896 Sequence

ALIGNMENTS

RESULT 1
AR016034
LOCUS AR016034 11 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 2 from patent US 5776679.
ACCESSION AR016034
VERSION AR016034.1 GI:3972311
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Assays for the DNA component of human telomerase
JOURNAL Patent: US 5776679-A 2 07-JUL-1998;
FEATURES Location/Qualifiers

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Qy          1 CTAACCCTAAC 11
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Db          1 CTAACCCTAAC 11


RESULT 2
AR026486/c
LOCUS       AR026486                  11 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 11 from patent US 5856096.
ACCESSION   AR026486
VERSION     AR026486.1  GI:5937326
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Windle,B.E., Qiu,M., Chen,S.-F., Fletcher,T.M. and Maine,I.
  TITLE     Rapid and sensitive assays for detecting and distinguishing between
            processive and non-processive telomerase activities
  JOURNAL   Patent: US 5856096-A 11 05-JAN-1999;
FEATURES             Location/Qualifiers
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BASE COUNT        2 a      0 c      5 g      4 t
ORIGIN

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  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||
Db         11 CTAACCCTAAC 1


RESULT 3
AR026487
LOCUS       AR026487                  11 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 12 from patent US 5856096.
ACCESSION   AR026487
VERSION     AR026487.1  GI:5937327
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Windle,B.E., Qiu,M., Chen,S.-F., Fletcher,T.M. and Maine,I.
  TITLE     Rapid and sensitive assays for detecting and distinguishing between
            processive and non-processive telomerase activities
  JOURNAL   Patent: US 5856096-A 12 05-JAN-1999;
FEATURES             Location/Qualifiers
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Qy          1 CTAACCCTAAC 11
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Db          1 CTAACCCTAAC 11


RESULT 4
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LOCUS       AR059195                  11 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2 from patent US 5837857.
ACCESSION   AR059195
VERSION     AR059195.1  GI:5984772
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
  TITLE     Mammalian telomerase
  JOURNAL   Patent: US 5837857-A 2 17-NOV-1998;
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Qy          1 CTAACCCTAAC 11
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Db          1 CTAACCCTAAC 11


RESULT 5
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LOCUS       AR075506                  11 bp    DNA     linear   PAT 30-AUG-2000
DEFINITION  Sequence 3 from patent US 5958680.
ACCESSION   AR075506
VERSION     AR075506.1  GI:10002256
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
  TITLE     Mammalian telomerase
  JOURNAL   Patent: US 5958680-A 3 28-SEP-1999;
FEATURES             Location/Qualifiers
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BASE COUNT        4 a      5 c      0 g      2 t
ORIGIN

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Qy          1 CTAACCCTAAC 11
              ||||||||||
Db          1 CTAACCCTAAC 11


RESULT 6
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LOCUS       AR161904                  11 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 2 from patent US 6258535.
ACCESSION   AR161904
VERSION     AR161904.1  GI:16228913
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
  TITLE     Mammalian telomerase
  JOURNAL   Patent: US 6258535-A 2 10-JUL-2001;
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FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 CTAACCCTAAC 11
              ||||||||||
Db          1 CTAACCCTAAC 11


RESULT 7
AX033373
LOCUS       AX033373                  11 bp    mRNA     linear   PAT 21-SEP-2000
DEFINITION  Sequence 5 from Patent WO0046601.
ACCESSION   AX033373
VERSION     AX033373.1  GI:10280147
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Larsen,F. and Skaanseng,M.
  TITLE     Detecting telomerase activity
  JOURNAL   Patent: WO 0046601-A 5 10-AUG-2000;
            LARSEN FRANK (NO) ; SKAANSENG MARIANNE (NO)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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Qy          1 CTAACCCTAAC 11
              ||||||||||
Db          1 CTAACCCTAAC 11


RESULT 8
AX268757/c
LOCUS       AX268757                  11 bp    DNA      linear   PAT 29-OCT-2001
DEFINITION  Sequence 5 from Patent WO0174342.
ACCESSION   AX268757
VERSION     AX268757.1  GI:16541829
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gilchrest,B.A., Yaar,M. and Eller,M.
  TITLE     Use of locally applied dna fragments
  JOURNAL   Patent: WO 0174342-A 5 11-OCT-2001;
            TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .11
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  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||
Db         11 CTAACCCTAAC 1


RESULT 9
AX268761
LOCUS       AX268761                  11 bp    DNA      linear   PAT 29-OCT-2001
DEFINITION  Sequence 9 from Patent WO0174342.
ACCESSION   AX268761
VERSION     AX268761.1  GI:16541833
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gilchrest,B.A., Yaar,M. and Eller,M.
  TITLE     Use of locally applied dna fragments
  JOURNAL   Patent: WO 0174342-A 9 11-OCT-2001;
            TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES             Location/Qualifiers
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Qy          1 CTAACCCTAAC 11
              ||||||||||
Db          1 CTAACCCTAAC 11


RESULT 10
AX283296/c
LOCUS       AX283296                  11 bp    DNA      linear   PAT 20-NOV-2001
DEFINITION  Sequence 60 from Patent WO0179249.
ACCESSION   AX283296
VERSION     AX283296.1  GI:17044177
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Uhlmann,E., Breipohl,G. and Will,D.W.
  TITLE     Polyamide nucleic acid derivatives, agents and methods for
            producing the same
  JOURNAL   Patent: WO 0179249-A 60 25-OCT-2001;
            Aventis Pharma Deutschland GmbH (DE)
FEATURES             Location/Qualifiers
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Qy          1 CTAACCCTAAC 11
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Db         11 CTAACCCTAAC 1


RESULT 11
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I31749
LOCUS       I31749                    11 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 2 from patent US 5583016.
ACCESSION   I31749
VERSION     I31749.1  GI:1822540
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
  TITLE     Mammalian telomerase
  JOURNAL   Patent: US 5583016-A 2 10-DEC-1996;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 CTAACCCTAAC 11
              ||||||||||| |
Db          1 CTAACCCTAAC 11


RESULT 12
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LOCUS       AR026479                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5856096.
ACCESSION   AR026479
VERSION     AR026479.1  GI:5937319
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Windle,B.E., Qiu,M., Chen,S.-F., Fletcher,T.M. and Maine,I.
  TITLE     Rapid and sensitive assays for detecting and distinguishing between
            processive and non-processive telomerase activities
  JOURNAL   Patent: US 5856096-A 4 05-JAN-1999;
FEATURES             Location/Qualifiers
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BASE COUNT        4 a      9 c      0 g      2 t
ORIGIN

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Qy          1 CTAACCCTAAC 11
              ||||||||||| |
Db          3 CTAACCCTAAC 13


RESULT 13
AR050942
LOCUS       AR050942                  16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 11 from patent US 5830644.
ACCESSION   AR050942
VERSION     AR050942.1  GI:5974306
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   West,M.D., Shay,J. and Wright,W.E.
  TITLE     Method for screening for agents which increase telomerase activity
            in a cell
  JOURNAL   Patent: US 5830644-A 11 03-NOV-1998;
FEATURES             Location/Qualifiers
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Qy          1 CTAACCCTAAC 11
              ||||||||||| |
Db          3 CTAACCCTAAC 13


RESULT 14
AR204610
LOCUS       AR204610                  16 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 60 from patent US 6368789.
ACCESSION   AR204610
VERSION     AR204610.1  GI:21501980
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   West,M.D., Shay,J., Wright,W. and Blackburn,E.H.
  TITLE     Screening methods to identify inhibitors of telomerase activity
  JOURNAL   Patent: US 6368789-A 60 09-APR-2002;
FEATURES             Location/Qualifiers
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BASE COUNT        4 a      9 c      0 g      3 t
ORIGIN

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Qy          1 CTAACCCTAAC 11
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Db          3 CTAACCCTAAC 13


RESULT 15
I51743
LOCUS       I51743                    16 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 11 from patent US 5645986.
ACCESSION   I51743
VERSION     I51743.1  GI:2472944
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   West,M.D., Harley,C.B., Strahl,C.M., McEachern,M.J., Shay,J.,
            Wright,W.E., Blackburn,E.H. and Vaziri,H.
  TITLE     Therapy and diagnosis of conditions related to telomere length
            and/or telomerase activity
  JOURNAL   Patent: US 5645986-A 11 08-JUL-1997;
FEATURES             Location/Qualifiers
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Qy          1 CTAACCCTAAC 11
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Db          3 CTAACCCTAAC 13
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GenCore version 5.1.6

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SUMMARIES

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c	4	11	100.0	11	18	AAT90060	Telomerase primer.
c	5	11	100.0	11	21	AAA37556	PNA sequence #13 u
c	6	11	100.0	11	21	AAA37561	PNA sequence #18 u
c	7	11	100.0	11	21	AAA37562	PNA sequence #19 u
	8	11	100.0	11	21	AAA37573	PNA sequence #31 u
c	9	11	100.0	11	21	AAA37586	Antisense sequence
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c	17	11	100.0	11	23	AAS15457	Phosphorothioate.(
c	18	11	100.0	11	24	AAK98619	Modified peptide n
c	19	11	100.0	11	24	ABA97513	Peptide nucleic ac
c	20	11	100.0	12	18	AAT89232	Peptide nucleic ac
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c	23	11	100.0	12	23	ABI05288	Oligonucleotide pr
	24	11	100.0	12	23	ABI34202	Oligonucleotide pr
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c	27	11	100.0	13	21	AAA37544	PNA sequence #1 us
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c	29	11	100.0	13	22	AAF81195	Thiophosphoramidat
c	30	11	100.0	13	23	AAS15423	PNA 8/VI inhibitin
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c	32	11	100.0	13	23	ABC19880	Oligonucleotide SE
	33	11	100.0	13	23	ABC19881	Oligonucleotide SE
c	34	11	100.0	13	23	ABF02802	Oligonucleotide SE
	35	11	100.0	13	23	ABF02803	Oligonucleotide SE
c	36	11	100.0	15	18	AAT89226	Peptide nucleic ac
c	37	11	100.0	15	18	AAT89229	Peptide nucleic ac
	38	11	100.0	15	18	AAT90068	Telomerase primer
c	39	11	100.0	15	21	AAA37545	PNA sequence #2 us
c	40	11	100.0	15	21	AAA37548	PNA sequence #5 us
c	41	11	100.0	15	21	AAA37587	Antisense sequence
c	42	11	100.0	15	23	AAS15424	PNA VII inhibiting
c	43	11	100.0	15	23	AAS15427	PNA XIII inhibitin
c	44	11	100.0	15	23	AAS15458	Phosphorothioate (
	45	11	100.0	16	16	AAT01177	Telomeric repeat-b

ALIGNMENTS

RESULT 1
AAV07769/c
ID AAV07769 standard; DNA; 11 BP.
XX
AC AAV07769;
XX
DT 07-DEC-1998 (first entry)
XX
DE N3 to P5 oligonucleotide phosphoramidate useful as telomerase inhibitor.
XX
KW telomerase inhibitor; phosphoramidate; telomerase-binding region; TBR;
KW cell proliferation; tumour; lukaemia; duplex; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..11
FT /*tag= a
FT /note= "each linkage is a phosphoramidate linkage"
XX
PN WO9737691-A1.
XX
PD 16-OCT-1997.
XX
PF 08-APR-1997; 97WO-US05773.
XX
PR 10-APR-1996; 96US-0630242.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
XX
PI Lloyd DH;
XX

DR WPI; 1997-512422/47.
XX
PT Treating elevated telomerase levels with N3 to P5 oligonucleotide
PT phosphoramidates - that bind to the RNA component of telomerase,
PT specifically for preventing growth of cancer cells, fungi and
PT protozoa
XX
PS Claim 5; Page 25; 38pp; English.
XX
CC The invention relates to treatment of conditions associated with high
CC levels of telomerase activity in a cell. The treatment comprises
CC administering an oligonucleotide N3' => P5' phosphoramidate having a
CC sequence complementary to part of the telomere-binding region (TBR) of
CC the RNA component of telomerase, so as to inhibit its activity. The
CC N3' => P5' oligonucleotide phosphoramidates are used therapeutically to
CC inhibit cell proliferation, e.g. against a wide range of solid tumours
CC or leukaemia, and also against fungal and protozoal pathogens. They are
CC soluble and resistant to nuclease, and they bind strongly to RNA forming
CC short but stable duplexes under physiological conditions. Thus they are
CC very effective and selective inhibitors of telomerase. The present
CC sequence represents a specific example of an oligonucleotide N3' => P5'
CC phosphoramidate disclosed in the specification.
XX
SQ Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 11; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAACCCTAAC 11
||||||||||||
Db 11 CTAACCCTAAC 1

RESULT 2
AAT89250
ID AAT89250 standard; DNA; 11 BP.
XX
AC AAT89250;
XX
DT 12-MAY-1998 (first entry)
XX
DE DNA oligonucleotide 6, used in the measurement of Tm values.
XX
KW Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
KW inhibitor; human telomerase RNA; hTR; PCR; oligonucleotide; ss.
XX
OS Synthetic.
XX
PN WO9738013-A1.
XX
PD 16-OCT-1997.
XX
PF 09-APR-1997; 97WO-US05931.
XX
PR 09-APR-1996; 96US-0630019.
XX
PA (GERO-) GERON CORP.
XX
PI Corey D, Norton JC, Piatyszek MA, Shay JW, Wright WE;
XX
DR WPI; 1997-512647/47.
XX
PT New peptide nucleic acids hybridising to mammalian telomerase RNA -
PT used to inhibit telomerase, for treating tumours and other
PT proliferative diseases, also for diagnosis
XX
PS Example 2; Page 49; 76pp; English.
XX
CC This is an oligonucleotide used in the measurement of Tm values and
CC their complimentary peptide nucleic acids (PNAs), (e.g.
CC AAT89231-T89240). PNAs hybridise specifically to an RNA component of
CC mammalian telomerase, and include the sequence GGG for specific
CC hybridisation to the template region of this component. PNAs can be used
CC as probes to detect the RNA component of mammalian telomerase and as
CC inhibitors of telomerase activity, especially in the treatment of
CC cancer.
XX
SQ Sequence 11 BP; 4 A; 5 C; 0 G; 2 T; 0 other;

Query Match 100.0%; Score 11; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAACCCTAAC 11
||||||||||||
Db 1 CTAACCCTAAC 11

RESULT 3
AAT89237/c
ID AAT89237 standard; DNA; 11 BP.
XX
AC AAT89237;
XX
DT 12-MAY-1998 (first entry)
XX
DE Peptide nucleic acid 12, targeted to mammalian telomerase.
XX
KW Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
KW inhibitor; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..13
FT /*tag= a
FT /note= "Sugar-phosphate backbone has been replaced by
FT a peptide backbone"
FT modified_base 1
FT /*tag= b
FT /note= "Optionally conjugated to peptide AAW31919"
FT modified_base 13
FT /*tag= c
FT /note= "Optionally conjugated to peptide AAW31919"
XX
PN WO9738013-A1.
XX
PD 16-OCT-1997.
XX
PF 09-APR-1997; 97WO-US05931.
XX
PR 09-APR-1996; 96US-0630019.
XX
PA (GERO-) GERON CORP.
XX
PI Corey D, Norton JC, Piatyszek MA, Shay JW, Wright WE;
XX
DR WPI; 1997-512647/47.
XX
PT New peptide nucleic acids hybridising to mammalian telomerase RNA -
PT used to inhibit telomerase, for treating tumours and other
PT proliferative diseases, also for diagnosis
XX
PS Claim 9; Page 59; 76pp; English.
XX
CC This sequence is a novel peptide nucleic acid (PNA), which acts as
CC an inhibitor of mammalian, preferably human, telomerase. The PNAs
CC hybridise specifically to an RNA component of mammalian telomerase,
CC and include the sequence GGG for specific hybridisation to the template
CC region of this component. PNAs can be used as probes to detect the
CC RNA component of mammalian telomerase and as inhibitors of telomerase
CC activity, especially in the treatment of cancer.
XX
SQ Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

```
  Query Match             100.0%;  Score 11;  DB 18;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||| 
Db         11 CTAACCCTAAC 1


RESULT 4
AAT90060/c
ID   AAT90060 standard; DNA; 11 BP.
XX
AC   AAT90060;
XX
DT   24-NOV-1997  (first entry)
XX
DE   Telomerase primer.
XX
KW   Detection; telomerase; amplification; polymerase chain reaction;
KW   PCR; primer; cancer; carcinoma; sarcoma; leukaemia; leukemia;
KW   myeloma; lymphoma; neuroblastoma; astrocytoma; glioma;
KW   glioblastoma; retinoblastoma; melanoma; screen; drug;
KW   determination; telomere length; ss.
XX
OS   Synthetic.
XX
PN   WO9711198-A1.
XX
PD   27-MAR-1997.
XX
PF   20-SEP-1996;   96WO-US15162.
XX
PR   20-SEP-1995;   95US-0531743.
XX
PA   (CTRC-) CTRC RES FOUND.
XX
PI   Chen S,  Fletcher TM,  Maine I,  Qiu M,  Windle BE;
XX
DR   WPI; 1997-202904/18.
XX
PT   Detecting telomerase activity by ligation sequential reaction -
PT   useful for diagnosis of cancer or to screen for telomerase
PT   inhibitors
XX
PS   Claim 40; Page 27; 71pp; English.
XX
CC   A novel method of detecting telomerase activity in a sample,
CC   comprises amplifying a sample with a telomerase primer, e.g. the
CC   present sequence, and contacting the product with 1st and 2nd
CC   oligonucleotides, which hybridise to the product so that no single
CC   stranded region intervenes between them. The hybridised product and
CC   oligonucleotides are then contacted with ligase and the ligated
CC   form of the oligonucleotides detected.
CC   The method can be used to detect cancer, e.g. carcinomas of the
CC   breast, colon, oesophagus, kidney, liver, lung, ovaries, prostate,
CC   stomach, uterus, pancreas and head and neck, sarcomas of bone and
CC   muscle, leukaemias, myelomas, lymphomas, neuroblastomas,
CC   astrocytomas, gliomas, glioblastomas, retinoblastomas and
CC   melanomas. The method can also be used to screen for
CC   anti-telomerase activity in candidate drugs and to determine
CC   telomere length.
XX
SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 18;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||| 
Db         11 CTAACCCTAAC 1


RESULT 5
AAA37556/c
ID   AAA37556 standard; DNA; 11 BP.
XX
AC   AAA37556;
XX
DT   15-AUG-2000  (first entry)
XX
DE   PNA sequence #13 used to inhibit telomerase activity.
XX
KW   Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
KW   inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
KW   AIDS; HIV; fungal infection; forensic identification; detect; tumour;
KW   paternity testing; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..11
FT                   /*tag= a
FT                   /note= "Peptide nucleic acid molecule, where
FT                          N-(2-aminoethyl)glycine units are linked to
FT                          nucleotide bases via glycine amino N through a
FT                          methylenecarbonyl linker"
XX
PN   US6046307-A.
XX
PD   04-APR-2000.
XX
PF   09-APR-1997;   97US-0838545.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Wright WE,  Piatyszek MA,  Shay JW,  Norton JC,  Corey DR;
XX
DR   WPI; 2000-292432/25.
XX
PT   New peptide nucleic acid (PNA) compounds that inhibit telomerase
PT   activity in mammalian cells is useful as probes to detect the RNA
PT   component of a mammalian telomerase  -
XX
PS   Claim 6; Column 71; 45pp; English.
XX
CC   The present sequence represents a peptide nucleic acid molecule which
CC   hybridises to the mRNA component of mammalian telomerase, and inhibits
CC   telomerase activity. Telomerase is a ribonucleoprotein enzyme that
CC   synthesizes one strand of the telomeric DNA, using as a template an 11
CC   nucleotide sequence contained within the RNA component of the enzyme. The
CC   invention relates to PNA molecules having a sequence of no more than 25
CC   bases, which include the sequence GTTAGG. The uncharged nature of the PNA
CC   backbone increases the melting temperature of associating strands,
CC   increases the rate of association with targeted nucleic acids, and
CC   affords greater resistance of degradation by proteases or nucleases. The
CC   therapeutic PNAs may be used for treating disease conditions such as
CC   cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
CC   immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
CC   syndrome) and associated pathologies, fungal infections, and other
CC   diseases characterized by abnormal telomere metabolism or telomerase
CC   activity, in combination with antineoplastic and other cytotoxic or
CC   cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
CC   used for molecular diagnostics, labelled PNAs are used as hybridization
CC   probes to detect or quantitate polynucleotides having a human telomerase
CC   RNA (hTR) sequence. PNA probes are also used for forensic identification
CC   of individuals, e.g. paternity testing, based on hTR gene restriction
CC   fragment length polymorphism (RFLP) pattern. PNAs are also useful as
CC   probes to detect the RNA component of a mammalian telomerase and as
CC   inhibitors of telomerase activity. The method of the present invention
CC   allows cancerous conditions to be detected with increased confidence and
CC   possibly at an earlier stage, before cells are detected as cancerous
CC   based on pathological characteristics. The diagnostic and prognostic
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CC   methods of the present invention can be used to detect an immortal or
CC   neoplastic cell or tumour tissue or cancer of any origin, provided the
CC   cell expresses telomerase activity and its RNA component.
XX
SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 21;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||
Db         11 CTAACCCTAAC 1


RESULT 6
AAA37561/c
ID   AAA37561 standard; DNA; 11 BP.
XX
AC   AAA37561;
XX
DT   15-AUG-2000  (first entry)
XX
DE   PNA sequence #18 used to inhibit telomerase activity.
XX
KW   Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
KW   inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
KW   AIDS; HIV; fungal infection; forensic identification; detect; tumour;
KW   paternity testing; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..11
FT                   /*tag=  a
FT                   /note= "Peptide nucleic acid molecule, where
FT                          N-(2-aminoethyl)glycine units are linked to
FT                          nucleotide bases via glycine amino N through a
FT                          methylenecarbonyl linker"
FT   misc_feature    1
FT                   /*tag=  b
FT                   /note= "G residue is linked to the carboxy end of the
FT                          peptide GGRQIKIWFQNNMKWKK"
XX
PN   US6046307-A.
XX
PD   04-APR-2000.
XX
PF   09-APR-1997;   97US-0838545.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Wright WE,  Piatyszek MA,  Shay JW,  Norton JC,  Corey DR;
XX
DR   WPI; 2000-292432/25.
XX
PT   New peptide nucleic acid (PNA) compounds that inhibit telomerase
PT   activity in mammalian cells is useful as probes to detect the RNA
PT   component of a mammalian telomerase  -
XX
PS   Claim 9; Column 71-72; 45pp; English.
XX
CC   The present sequence represents a peptide nucleic acid molecule which
CC   hybridises to the mRNA component of mammalian telomerase, and inhibits
CC   telomerase activity. Telomerase is a ribonucleoprotein enzyme that
CC   synthesizes one strand of the telomeric DNA, using as a template an 11
CC   nucleotide sequence contained within the RNA component of the enzyme. The
CC   invention relates to PNA molecules having a sequence of no more than 25
CC   bases, which include the sequence GTTAGG. The uncharged nature of the PNA
CC   backbone increases the melting temperature of associating strands,
CC   increases the rate of association with targeted nucleic acids, and
CC   affords greater resistance of degradation by proteases or nucleases. The
CC   therapeutic PNAs may be used for treating disease conditions such as
CC   cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
CC   immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
CC   syndrome) and associated pathologies, fungal infections, and other
CC   diseases characterized by abnormal telomere metabolism or telomerase
CC   activity, in combination with antineoplastic and other cytotoxic or
CC   cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
CC   used for molecular diagnostics, labelled PNAs are used as hybridization
CC   probes to detect or quantitate polynucleotides having a human telomerase
CC   RNA (hTR) sequence. PNA probes are also used for forensic identification
CC   of individuals, e.g. paternity testing, based on hTR gene restriction
CC   fragment length polymorphism (RFLP) pattern. PNAs are also useful as
CC   probes to detect the RNA component of a mammalian telomerase and as
CC   inhibitors of telomerase activity. The method of the present invention
CC   allows cancerous conditions to be detected with increased confidence and
CC   possibly at an earlier stage, before cells are detected as cancerous
CC   based on pathological characteristics. The diagnostic and prognostic
CC   methods of the present invention can be used to detect an immortal or
CC   neoplastic cell or tumour tissue or cancer of any origin, provided the
CC   cell expresses telomerase activity and its RNA component.
XX
SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 21;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||
Db         11 CTAACCCTAAC 1


RESULT 7
AAA37562/c
ID   AAA37562 standard; DNA; 11 BP.
XX
AC   AAA37562;
XX
DT   15-AUG-2000  (first entry)
XX
DE   PNA sequence #19 used to inhibit telomerase activity.
XX
KW   Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
KW   inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
KW   AIDS; HIV; fungal infection; forensic identification; detect; tumour;
KW   paternity testing; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..11
FT                   /*tag=  a
FT                   /note= "Peptide nucleic acid molecule, where
FT                          N-(2-aminoethyl)glycine units are linked to
FT                          nucleotide bases via glycine amino N through a
FT                          methylenecarbonyl linker"
FT   misc_feature    11
FT                   /*tag=  b
FT                   /note= "G residue is linked to the amino end of the
FT                          peptide GGRQIKIWFQNNMKWKK"
XX
PN   US6046307-A.
XX
PD   04-APR-2000.
XX
PF   09-APR-1997;   97US-0838545.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Wright WE,  Piatyszek MA,  Shay JW,  Norton JC,  Corey DR;
```

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XX
DR   WPI; 2000-292432/25.
XX
PT   New peptide nucleic acid (PNA) compounds that inhibit telomerase
PT   activity in mammalian cells is useful as probes to detect the RNA
PT   component of a mammalian telomerase  -
XX
PS   Claim 9; Column 71-72; 45pp; English.
XX
CC   The present sequence represents a peptide nucleic acid molecule which
CC   hybridises to the mRNA component of mammalian telomerase, and inhibits
CC   telomerase activity. Telomerase is a ribonucleoprotein enzyme that
CC   synthesizes one strand of the telomeric DNA, using as a template an 11
CC   nucleotide sequence contained within the RNA component of the enzyme. The
CC   invention relates to PNA molecules having a sequence of no more than 25
CC   bases, which include the sequence GTTAGG. The uncharged nature of the PNA
CC   backbone increases the melting temperature of associating strands,
CC   increases the rate of association with targeted nucleic acids, and
CC   affords greater resistance of degradation by proteases or nucleases. The
CC   therapeutic PNAs may be used for treating disease conditions such as
CC   cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
CC   immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
CC   syndrome) and associated pathologies, fungal infections, and other
CC   diseases characterized by abnormal telomere metabolism or telomerase
CC   activity, in combination with antineoplastic and other cytotoxic or
CC   cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
CC   used for molecular diagnostics, labelled PNAs are used as hybridization
CC   probes to detect or quantitate polynucleotides having a human telomerase
CC   RNA (hTR) sequence. PNA probes are also used for forensic identification
CC   of individuals, e.g. paternity testing, based on hTR gene restriction
CC   fragment length polymorphism (RFLP) pattern. PNAs are also useful as
CC   probes to detect the RNA component of a mammalian telomerase and as
CC   inhibitors of telomerase activity. The method of the present invention
CC   allows cancerous conditions to be detected with increased confidence and
CC   possibly at an earlier stage, before cells are detected as cancerous
CC   based on pathological characteristics. The diagnostic and prognostic
CC   methods of the present invention can be used to detect an immortal or
CC   neoplastic cell or tumour tissue or cancer of any origin, provided the
CC   cell expresses telomerase activity and its RNA component.
XX
SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 21;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||| |
Db         11 CTAACCCTAAC 1


RESULT 8
AAA37573
ID   AAA37573 standard; DNA; 11 BP.
XX
AC   AAA37573;
XX
DT   15-AUG-2000  (first entry)
XX
DE   PNA sequence #31 used to inhibit telomerase activity.
XX
KW   Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
KW   inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
KW   AIDS; HIV; fungal infection; forensic identification; detect; tumour;
KW   paternity testing; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..11
FT                   /*tag=  a
FT                   /note= "Peptide nucleic acid molecule, where
FT                          N-(2-aminoethyl)glycine units are linked to
FT                          nucleotide bases via glycine amino N through a
FT                          methylenecarbonyl linker"
XX
PN   US6046307-A.
XX
PD   04-APR-2000.
XX
PF   09-APR-1997;   97US-0838545.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Wright WE,  Piatyszek MA,  Shay JW,  Norton JC,  Corey DR;
XX
DR   WPI; 2000-292432/25.
XX
PT   New peptide nucleic acid (PNA) compounds that inhibit telomerase
PT   activity in mammalian cells is useful as probes to detect the RNA
PT   component of a mammalian telomerase  -
XX
PS   Example 2; Column 33; 45pp; English.
XX
CC   The present sequence represents a peptide nucleic acid molecule which
CC   hybridises to the mRNA component of mammalian telomerase, and inhibits
CC   telomerase activity. Telomerase is a ribonucleoprotein enzyme that
CC   synthesizes one strand of the telomeric DNA, using as a template an 11
CC   nucleotide sequence contained within the RNA component of the enzyme. The
CC   invention relates to PNA molecules having a sequence of no more than 25
CC   bases, which include the sequence GTTAGG. The uncharged nature of the PNA
CC   backbone increases the melting temperature of associating strands,
CC   increases the rate of association with targeted nucleic acids, and
CC   affords greater resistance of degradation by proteases or nucleases. The
CC   therapeutic PNAs may be used for treating disease conditions such as
CC   cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
CC   immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
CC   syndrome) and associated pathologies, fungal infections, and other
CC   diseases characterized by abnormal telomere metabolism or telomerase
CC   activity, in combination with antineoplastic and other cytotoxic or
CC   cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
CC   used for molecular diagnostics, labelled PNAs are used as hybridization
CC   probes to detect or quantitate polynucleotides having a human telomerase
CC   RNA (hTR) sequence. PNA probes are also used for forensic identification
CC   of individuals, e.g. paternity testing, based on hTR gene restriction
CC   fragment length polymorphism (RFLP) pattern. PNAs are also useful as
CC   probes to detect the RNA component of a mammalian telomerase and as
CC   inhibitors of telomerase activity. The method of the present invention
CC   allows cancerous conditions to be detected with increased confidence and
CC   possibly at an earlier stage, before cells are detected as cancerous
CC   based on pathological characteristics. The diagnostic and prognostic
CC   methods of the present invention can be used to detect an immortal or
CC   neoplastic cell or tumour tissue or cancer of any origin, provided the
CC   cell expresses telomerase activity and its RNA component.
XX
SQ   Sequence 11 BP; 4 A; 5 C; 0 G; 2 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 21;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||| |
Db          1 CTAACCCTAAC 11


RESULT 9
AAA37586/c
ID   AAA37586 standard; DNA; 11 BP.
XX
AC   AAA37586;
XX
DT   15-AUG-2000  (first entry)
XX
```

```
DE   Antisense sequence #44 used to inhibit telomerase activity.
XX
KW   Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
KW   inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
KW   AIDS; HIV; fungal infection; forensic identification; detect; tumour;
KW   paternity testing; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..11
FT                   /*tag= a
FT                   /note= "Phosphorothioate internucleotide linkages"
XX
PN   US6046307-A.
XX
PD   04-APR-2000.
XX
PF   09-APR-1997;   97US-0838545.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Wright WE,  Piatyszek MA,  Shay JW,  Norton JC,  Corey DR;
XX
DR   WPI; 2000-292432/25.
XX
PT   New peptide nucleic acid (PNA) compounds that inhibit telomerase
PT   activity in mammalian cells is useful as probes to detect the RNA
PT   component of a mammalian telomerase  -
XX
PS   Example 1; Column 27-28; 45pp; English.
XX
CC   The present sequence represents an antisense oligonucleotide used as a
CC   control sequence alongside a peptide nucleic acid molecule which
CC   hybridises to the mRNA component of mammalian telomerase, and inhibits
CC   telomerase activity. Telomerase is a ribonucleoprotein enzyme that
CC   synthesizes one strand of the telomeric DNA, using as a template an 11
CC   nucleotide sequence contained within the RNA component of the enzyme. The
CC   invention relates to PNA molecules having a sequence of no more than 25
CC   bases, which include the sequence GTTAGG. The uncharged nature of the PNA
CC   backbone increases the melting temperature of associating strands,
CC   increases the rate of association with targeted nucleic acids, and
CC   affords greater resistance of degradation by proteases or nucleases. The
CC   therapeutic PNAs may be used for treating disease conditions such as
CC   cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
CC   immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
CC   syndrome) and associated pathologies, fungal infections, and other
CC   diseases characterized by abnormal telomere metabolism or telomerase
CC   activity, in combination with antineoplastic and other cytotoxic or
CC   cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
CC   used for molecular diagnostics, labelled PNAs are used as hybridization
CC   probes to detect or quantitate polynucleotides having a human telomerase
CC   RNA (hTR) sequence. PNA probes are also used for forensic identification
CC   of individuals, e.g. paternity testing, based on hTR gene restriction
CC   fragment length polymorphism (RFLP) pattern. PNAs are also useful as
CC   probes to detect the RNA component of a mammalian telomerase and as
CC   inhibitors of telomerase activity. The method of the present invention
CC   allows cancerous conditions to be detected with increased confidence and
CC   possibly at an earlier stage, before cells are detected as cancerous
CC   based on pathological characteristics. The diagnostic and prognostic
CC   methods of the present invention can be used to detect an immortal or
CC   neoplastic cell or tumour tissue or cancer of any origin, provided the
CC   cell expresses telomerase activity and its RNA component.
XX
SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 21;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||| |
Db         11 CTAACCCTAAC 1


RESULT 10
AAF81185/c
ID   AAF81185 standard; DNA; 11 BP.
XX
AC   AAF81185;
XX
DT   30-MAY-2001  (first entry)
XX
DE   Oligonucleotide thiophosphoramidate, SEQ ID NO: 1.
XX
KW   Thiophosphoramidate oligonucleotide; virucide; cytostatic;
KW   immunosuppressive; contraceptive; RNA inhibitor; telomerase inhibitor;
KW   antisense therapy; viral infection; cancer; hyperproliferative disorder;
KW   autoimmune disorder; ss.
XX
OS   Synthetic.
XX
PN   WO200118015-A1.
XX
PD   15-MAR-2001.
XX
PF   08-SEP-2000; 2000WO-US24688.
XX
PR   10-SEP-1999;   99US-0153201.
PR   19-OCT-1999;   99US-0160444.
XX
PA   (GERO-) GERON CORP.
XX
PI   Gryaznov S,  Pongracz K,  Matray T;
XX
DR   WPI; 2001-265967/27.
XX
PT   Novel thiophosphoramidate polynucleotide useful for detection of RNA or
PT   DNA having a given target sequence, for inhibiting RNA function in a
PT   cell, and for treating cancer and viral infection  -
XX
PS   Example 3; Page 39; 68pp; English.
XX
CC   The present sequence was synthesised in an example illustrating an
CC   invention relating to polynucleotides comprising a non-homopolymeric
CC   sequence of nucleoside subunits joined by at least one inter-subunit
CC   linkage that is a N3'-P5' thiophosphoramidate. The thiophosphoramidate
CC   oligonucleotides retain a high RNA binding affinity and exhibit a much
CC   higher acid stability. They are useful for detecting a specific sequence
CC   in a sample, by forming a hybridisation complex with the sequence. They
CC   are useful for inhibiting function of an RNA in a cell (for inhibiting
CC   translation of a mRNA or for inhibiting telomerase enzyme in a cell).
CC   They are also useful in the preparation of a medicament for treatment of
CC   viral infection or cancer. The oligonucleotides are useful for anti-sense
CC   and anti-gene diagnostic or therapeutic applications and may be used for
CC   treating telomerase-mediated conditions or diseases, such as
CC   hyperproliferative and autoimmune disorders, and for contraceptive
CC   purposes.
XX
SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 22;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||| |
Db         11 CTAACCCTAAC 1


RESULT 11
AAH26728/c
ID   AAH26728 standard; DNA; 11 BP.
XX
```

```
AC   AAH26728;
XX
DT   26-NOV-2001  (first entry)
XX
DE   Phosphoramidate-linked 2'-arabino-fluorooligonucleotide.
XX
KW   2'-arabino-fluorooligonucleotide; phosphoramidate; telomerase;
KW   inhibitor; infection; cancer; diagnosis; therapy; cytostatic;
KW   virucide; antisense; antigene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   2..11
FT                   /*tag=  a
FT                   /mod_base= "OTHER"
FT                   /note= "2'-arabino-fluoronucleosides"
FT   modified_base   2..11
FT                   /*tag=  b
FT                   /mod_base= "OTHER"
FT                   /note= "phosphoramidate linkage"
XX
PN   WO200153307-A1.
XX
PD   26-JUL-2001.
XX
PF   19-JAN-2001; 2001WO-US01918.
XX
PR   21-JAN-2000; 2000US-178248P.
XX
PA   (GERO-) GERON CORP.
XX
PI   Gryaznov S,  Schultz RG;
XX
DR   WPI; 2001-589652/66.
XX
PT   Polynucleotides, used to detect and isolate nucleic acids, inhibit
PT   function of RNA and telomerase enzymes and to treat e.g. viral
PT   infections, contain 2'-arabino-fluoronucleoside(s) linked to
PT   nucleoside(s) -
XX
PS   Example 6; Page 46; 61pp; English.
XX
CC   The present sequence is that of a N3'-P5' 2'-arabino-fluoro
CC   phosphoramidate oligonucleotide that is complementary to
CC   telomerase RNA.  The oligonucleotide was used to assess the
CC   relative efficacy of novel 2'-arabino-fluoro phosphoramidate
CC   oligonucleotides and their 2'-ribo fluorooligonucleotide
CC   counterparts (see AAH26728-35) for the inhibition of telomerase
CC   activity.  Novel phosphoramidate 2'-arabino-fluorooligonucleotides
CC   are generally more acid stable, more resistant to cellular
CC   proteases, and also show greater telomerase inhibition activity
CC   than 2'-ribose-fluoro phosphoramidates.  They are therefore useful
CC   for treating cancer (claimed) and other diseases in which telomerase
CC   activity is present at abnormal levels, such as hyperproliferative
CC   or autoimmune diseases e.g. psoriasis, rheumatoid arthritis,
CC   immune system disorders requiring immunosuppression, and in the
CC   treatment of viral infection (claimed).
XX
SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 22;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||| |
Db         11 CTAACCCTAAC 1


RESULT 12
AAH26732/c
ID   AAH26732 standard; DNA; 11 BP.
XX
AC   AAH26732;
XX
DT   26-NOV-2001  (first entry)
XX
DE   Phosphoramidate-linked 2'-ribose-fluorooligonucleotide.
XX
KW   2'-ribose-fluorooligonucleotide; phosphoramidate; telomerase;
KW   inhibitor; infection; cancer; diagnosis; therapy; cytostatic;
KW   virucide; antisense; antigene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   2..11
FT                   /*tag=  a
FT                   /mod_base= "OTHER"
FT                   /note= "2'-ribose-fluoronucleosides"
FT   modified_base   2..11
FT                   /*tag=  b
FT                   /mod_base= "OTHER"
FT                   /note= "phosphoramidate linkage"
XX
PN   WO200153307-A1.
XX
PD   26-JUL-2001.
XX
PF   19-JAN-2001; 2001WO-US01918.
XX
PR   21-JAN-2000; 2000US-178248P.
XX
PA   (GERO-) GERON CORP.
XX
PI   Gryaznov S,  Schultz RG;
XX
DR   WPI; 2001-589652/66.
XX
PT   Polynucleotides, used to detect and isolate nucleic acids, inhibit
PT   function of RNA and telomerase enzymes and to treat e.g. viral
PT   infections, contain 2'-arabino-fluoronucleoside(s) linked to
PT   nucleoside(s) -
XX
PS   Example 6; Page 46; 61pp; English.
XX
CC   The present sequence is that of a 2'-ribose-fluoro
CC   phosphoramidate oligonucleotide that is complementary to
CC   telomerase RNA.  The oligonucleotide was used to assess the
CC   relative efficacy of novel 2'-arabino-fluoro phosphoramidate
CC   oligonucleotides and their 2'-ribose fluorooligonucleotide
CC   counterparts (see AAH26728-35) for the inhibition of telomerase
CC   activity.  Novel phosphoramidate 2'-arabino-fluorooligonucleotides
CC   are generally more acid stable, more resistant to cellular
CC   proteases, and also show greater telomerase inhibition activity
CC   than 2'-ribose-fluoro phosphoramidates.  They are therefore useful
CC   for treating cancer (claimed) and other diseases in which telomerase
CC   activity is present at abnormal levels, such as hyperproliferative
CC   or autoimmune diseases e.g. psoriasis, rheumatoid arthritis,
CC   immune system disorders requiring immunosuppression, and in the
CC   treatment of viral infection (claimed).
XX
SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 22;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||| |
Db         11 CTAACCCTAAC 1


RESULT 13
AAS14909/c
```

```
ID   AAS14909 standard; DNA; 11 BP.
XX
AC   AAS14909;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Melanogenesis associated oligonucleotide #5.
XX
KW   Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW   anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW   immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW   tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW   carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW   conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag= a
FT                   /mod_base= g
FT                   /note= "Optionally phosphorylated"
FT   modified_base   1..11
FT                   /*tag= b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Optionally phosphorothiolate linkages"
XX
PN   WO200174342-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US10162.
XX
PR   31-MAR-2000; 2000US-0540843.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Gilchrest BA,  Yaar M,  Eller M;
XX
DR   WPI; 2001-626338/72.
XX
PT   Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT   carcinoma, using specific oligonucleotides that mimic the effects of
PT   ultra-violet light  -
XX
PS   Claim 1; Page 37; 74pp; English.
XX
CC   The invention describes inhibition of mammalian epithelial cell
CC   proliferation by treating cells with at least one oligonucleotide, or
CC   its fragment. The compounds, which have cytostatic, anti-allergic,
CC   anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC   immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC   DNA repair processes (or a protective response to later exposure to
CC   radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC   or a tumour necrosis factor inhibitor. Probably they mimic products of
CC   DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC   pathway, resulting in transient arrest of cell growth, allowing more time
CC   for DNA repair to occur before cell division takes place. The method is
CC   especially used to treat carcinoma but may also be used to: treat other
CC   hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC   reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC   allergically mediated inflammation (atopic or contact dermatitis,
CC   allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC   cells caused by radiation or chemicals; increase melanin production
CC   (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC   promote apoptosis in epithelial cells that contain damaged DNA. Also
CC   oligonucleotides that contain non-hydrolyzable backbones are used to
CC   inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC   sequence is melanogenesis associated oligonucleotide #5, representative
CC   of the telomere over-hang sequence and one of the oligonucleotides used
CC   to inhibit mammalian epithelial cell proliferation, described in the
CC   method of the invention.
XX

SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

  Query Match           100.0%;  Score 11;  DB 23;  Length 11;
  Best Local Similarity 100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||
Db         11 CTAACCCTAAC 1


RESULT 14
AAS14913
ID   AAS14913 standard; DNA; 11 BP.
XX
AC   AAS14913;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Melanogenesis associated oligonucleotide #9.
XX
KW   Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW   anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW   immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW   tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW   carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW   conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag= a
FT                   /mod_base= c
FT                   /note= "Phosphorylated"
XX
PN   WO200174342-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US10162.
XX
PR   31-MAR-2000; 2000US-0540843.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Gilchrest BA,  Yaar M,  Eller M;
XX
DR   WPI; 2001-626338/72.
XX
PT   Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT   carcinoma, using specific oligonucleotides that mimic the effects of
PT   ultra-violet light  -
XX
PS   Example 12; Page 37; 74pp; English.
XX
CC   The invention describes inhibition of mammalian epithelial cell
CC   proliferation by treating cells with at least one oligonucleotide, or
CC   its fragment. The compounds, which have cytostatic, anti-allergic,
CC   anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC   immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC   DNA repair processes (or a protective response to later exposure to
CC   radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC   or a tumour necrosis factor inhibitor. Probably they mimic products of
CC   DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC   pathway, resulting in transient arrest of cell growth, allowing more time
CC   for DNA repair to occur before cell division takes place. The method is
CC   especially used to treat carcinoma but may also be used to: treat other
CC   hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC   reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC   allergically mediated inflammation (atopic or contact dermatitis,
CC   allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC   cells caused by radiation or chemicals; increase melanin production
```

```
CC   (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC   promote apoptosis in epithelial cells that contain damaged DNA. Also
CC   oligonucleotides that contain non-hydrolyzable backbones are used to
CC   inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC   sequence is melanogenesis associated oligonucleotide #9, one of the
CC   oligonucleotides used to inhibit mammalian epithelial cell proliferation,
CC   described in the method of the invention.
XX
SQ   Sequence 11 BP; 4 A; 5 C; 0 G; 2 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 23;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||| 
Db          1 CTAACCCTAAC 11


RESULT 15
AAS15434/c
ID   AAS15434 standard; DNA; 11 BP.
XX
AC   AAS15434;
XX
DT   14-FEB-2002  (first entry)
XX
DE   PNA 7/IV inhibiting human and mammalian telomerase activity.
XX
KW   Mammalian; peptide nucleic acid; probe; forensic; paternity testing;
KW   human telomerase RNA component; hTR gene RFLP pattern; cancer;
KW   inflammation; lymphoproliferative disease; autoimmune disease;
KW   neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS;
KW   human immunodeficiency virus; acquired immunodeficiency syndrome;
KW   telomere metabolism; mutant; cytostatic; anti-inflammatory;
KW   immunosuppressive; polyamide backbone; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..11
FT                   /*tag=  a
FT                   /note= "This sequence is a peptide nucleic acid, i.e. it
FT                          contains a polyamide backbone instead of a
FT                          deoxyribose backbone"
XX
PN   US6294650-B1.
XX
PD   25-SEP-2001.
XX
PF   08-JUL-1999;   99US-0349532.
XX
PR   09-APR-1997;   97US-0838545.
PR   09-APR-1996;   96US-0630019.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Shay JW,  Wright WE,  Piatyszek MA,  Corey DR,  Norton JC;
XX
DR   WPI; 2001-638024/73.
XX
PT   New peptide nucleic acids that hybridizes to the RNA component of
PT   mammalian telomerase, useful for treating or preventing cancer,
PT   inflammation, lymphoproliferative diseases, autoimmune disease, or
PT   neurodegenerative diseases  -
XX
PS   Claim 7; Column 73; 46pp; English.
XX
CC   The present invention relates to peptide nucleic acids (PNAs), comprising
CC   a sequence of 6-25 nucleobases, that inhibit telomerase activity in
CC   mammalian cells by hybridising to the RNA component of mammalian
CC   telomerase. The PNAs are useful as probes to detect the RNA component
CC   of mammalian telomerase and as inhibitors of telomerase activity, or to
CC   detect and/or quantitate polynucleotide having the human telomerase
CC   RNA component (hTR) sequence, as well as in forensic identification of
CC   individuals, such as paternity testing or identification of criminal
CC   suspects or unknown descendants based on the hTR gene RFLP pattern. The
CC   PNA can be further used for treating or preventing cancer, inflammation,
CC   lymphoproliferative diseases, autoimmune disease, or neurodegenerative
CC   diseases. The PNAs in combination with other pharmaceuticals (such as
CC   antineoplastic or cytostatic agents) can be used for treating neoplasia,
CC   hyperplasia, human immunodeficiency virus (HIV) infections, acquired
CC   immunodeficiency syndrome (AIDS) and associated pathologies, and other
CC   diseases characterised by abnormal telomere metabolism or telomerase
CC   activity. The present sequence represents one of the PNA sequences
CC   of the invention.
XX
SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 23;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||| 
Db         11 CTAACCCTAAC 1


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GenCore version 5.1.6

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Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 558892

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	11	100.0	11	1	US-08-330-123A-2	Sequence 2, Appli
	2	11	100.0	11	1	US-08-482-115B-2	Sequence 2, Appli
	3	11	100.0	11	2	US-08-660-678A-2	Sequence 2, Appli
c	4	11	100.0	11	2	US-08-531-743-11	Sequence 11, Appl
	5	11	100.0	11	2	US-08-531-743-12	Sequence 12, Appl
	6	11	100.0	11	2	US-08-485-778-36	Sequence 36, Appl
	7	11	100.0	11	2	US-08-472-802C-3	Sequence 3, Appli
	8	11	100.0	11	3	US-08-520-550A-36	Sequence 36, Appl
c	9	11	100.0	11	3	US-08-630-019A-9	Sequence 9, Appli
	10	11	100.0	11	3	US-08-630-019A-30	Sequence 30, Appl
c	11	11	100.0	11	3	US-08-630-019A-39	Sequence 39, Appl
c	12	11	100.0	11	3	US-08-838-545-13	Sequence 13, Appl
	13	11	100.0	11	3	US-08-838-545-31	Sequence 31, Appl
c	14	11	100.0	11	3	US-08-838-545-44	Sequence 44, Appl
	15	11	100.0	11	3	US-08-998-443-2	Sequence 2, Appli
	16	11	100.0	11	4	US-09-060-523-2	Sequence 2, Appli
c	17	11	100.0	11	4	US-09-349-532-13	Sequence 13, Appl
	18	11	100.0	11	4	US-09-349-532-31	Sequence 31, Appl
c	19	11	100.0	11	4	US-09-349-532-44	Sequence 44, Appl
	20	11	100.0	11	4	US-09-580-517-2	Sequence 2, Appli
c	21	11	100.0	12	3	US-08-630-019A-10	Sequence 10, Appl
c	22	11	100.0	12	3	US-08-838-545-8	Sequence 8, Appli
c	23	11	100.0	12	4	US-09-349-532-8	Sequence 8, Appli
c	24	11	100.0	13	3	US-08-630-019A-11	Sequence 11, Appl
c	25	11	100.0	13	3	US-08-630-019A-15	Sequence 15, Appl
c	26	11	100.0	13	3	US-08-838-545-1	Sequence 1, Appli
c	27	11	100.0	13	3	US-08-838-545-12	Sequence 12, Appl
c	28	11	100.0	13	4	US-09-349-532-1	Sequence 1, Appli
c	29	11	100.0	13	4	US-09-349-532-12	Sequence 12, Appl
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c	31	11	100.0	15	3	US-08-630-019A-12	Sequence 12, Appl
c	32	11	100.0	15	3	US-08-630-019A-18	Sequence 18, Appl
c	33	11	100.0	15	3	US-08-630-019A-40	Sequence 40, Appl
c	34	11	100.0	15	3	US-08-838-545-2	Sequence 2, Appli
c	35	11	100.0	15	3	US-08-838-545-5	Sequence 5, Appli
c	36	11	100.0	15	3	US-08-838-545-45	Sequence 45, Appl
c	37	11	100.0	15	4	US-09-349-532-2	Sequence 2, Appli
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	41	11	100.0	16	2	US-08-151-477A-11	Sequence 11, Appl
	42	11	100.0	16	3	US-08-819-867-20	Sequence 20, Appl
	43	11	100.0	16	4	US-08-464-011B-60	Sequence 60, Appl
c	44	11	100.0	17	2	US-08-531-743-13	Sequence 13, Appl
	45	11	100.0	17	4	US-08-857-721-12	Sequence 12, Appl

ALIGNMENTS

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RESULT 1
US-08-330-123A-2
; Sequence 2, Application US/08330123A
; Patent No. 5583016
;  GENERAL INFORMATION:
;    APPLICANT:  VILLEPONTEAU, Bryant
;    APPLICANT:  FENG, Junli
;    APPLICANT:  FUNK, Walter
;    APPLICANT:  ANDREWS, William H.
;    TITLE OF INVENTION:  HUMAN TELOMERASE
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/330,123A
;      FILING DATE:  27-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15389-000810
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
US-08-330-123A-2

  Query Match           100.0%;  Score 11;  DB 1;  Length 11;
  Best Local Similarity  81.8%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 CTAACCCTAAC 11
              |:|||||:|||
Db          1 CUAACCCUAAC 11


RESULT 2
US-08-482-115B-2
; Sequence 2, Application US/08482115B
; Patent No. 5776679
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  Assays for the RNA Component of Human
;    TITLE OF INVENTION:  Telomerase
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,115B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-000830US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
US-08-482-115B-2

  Query Match             100.0%;  Score 11;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              |:|||||:|||
Db          1 CUAACCCUAAC 11


RESULT 3
US-08-660-678A-2
; Sequence 2, Application US/08660678A
; Patent No. 5837857
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  Mammalian Telomerase
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/660,678A
;      FILING DATE:  05-JUN-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-000811US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
US-08-660-678A-2

  Query Match             100.0%;  Score 11;  DB 2;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              |:|||||:|||
Db          1 CUAACCCUAAC 11


RESULT 4
US-08-531-743-11/c
; Sequence 11, Application US/08531743
; Patent No. 5856096
;  GENERAL INFORMATION:
;    APPLICANT:  Windle, Bradford E.
;    APPLICANT:  Qiu, Ming
;    APPLICANT:  Chen, Shi-fong
;    APPLICANT:  Fletcher, Terace M.
;    APPLICANT:  Maine, Ira
;    TITLE OF INVENTION:  Rapid and Sensitive Assays for Detecting and
;    TITLE OF INVENTION:  Distinguishing Between Processive and
;    TITLE OF INVENTION:  No. 5856096-Processive Telomerase Activities
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/531,743
;       FILING DATE:  20-SEP-1995
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Highlander, Steven L.
;       REGISTRATION NUMBER:  37,642
;       REFERENCE/DOCKET NUMBER:  CTRC:026/HYL
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (512) 418-3000
;       TELEFAX:  (512) 474-7577
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  11 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-531-743-11

  Query Match             100.0%;  Score 11;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||| 
Db         11 CTAACCCTAAC 1


RESULT 5
US-08-531-743-12
; Sequence 12, Application US/08531743
; Patent No. 5856096
;  GENERAL INFORMATION:
;    APPLICANT:  Windle, Bradford E.
;    APPLICANT:  Qiu, Ming
;    APPLICANT:  Chen, Shi-fong
;    APPLICANT:  Fletcher, Terace M.
;    APPLICANT:  Maine, Ira
;    TITLE OF INVENTION:  Rapid and Sensitive Assays for Detecting and
;    TITLE OF INVENTION:  Distinguishing Between Processive and
;    TITLE OF INVENTION:  No. 5856096-Processive Telomerase Activities
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/531,743
;      FILING DATE:  20-SEP-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Highlander, Steven L.
;      REGISTRATION NUMBER:  37,642
;      REFERENCE/DOCKET NUMBER:  CTRC:026/HYL
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-531-743-12

  Query Match             100.0%;  Score 11;  DB 2;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              |:|||||:|||
Db          1 CUAACCCUAAC 11


RESULT 6
US-08-485-778-36
; Sequence 36, Application US/08485778
; Patent No. 5876979
;  GENERAL INFORMATION:
;    APPLICANT:  Andrews, William H.
;    APPLICANT:  Avilion, Ariel Athena
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Greider, Carol
;    APPLICANT:  Marhuenda, Maria Antonia Blasco
;    APPLICANT:  Villeponteau, Bryant
;    TITLE OF INVENTION:  RNA COMPONENT OF TELOMERASE
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,778
;      FILING DATE:  07-JE-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/387,524
;      FILING DATE:  13-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  CSHL94-05A4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-485-778-36

  Query Match             100.0%;  Score 11;  DB 2;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              |:|||||:|||
Db          1 CUAACCCUAAC 11
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RESULT 7
US-08-472-802C-3
; Sequence 3, Application US/08472802C
; Patent No. 5958680
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  Mammalian Telomerase
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,802C
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15389-000820
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
US-08-472-802C-3

  Query Match             100.0%;  Score 11;  DB 2;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              |:||||:|||
Db          1 CUAACCCUAAC 11


RESULT 8
US-08-520-550A-36
; Sequence 36, Application US/08520550A
; Patent No. 6013468
;  GENERAL INFORMATION:
;    APPLICANT:  Andrews, William H.
;    APPLICANT:  Avilion, Ariel A.
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Greider, Carol
;    APPLICANT:  Marhuenda, Maria A. B.
;    APPLICANT:  Villeponteau, Bryant
;    TITLE OF INVENTION:  RNA Component of Telomerase
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/520,550A
;      FILING DATE:  29-AUG-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/387,524
;      FILING DATE:  13-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  CSHL94-05A3B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-520-550A-36

  Query Match             100.0%;  Score 11;  DB 3;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              |:||||:|||
Db          1 CUAACCCUAAC 11


RESULT 9
US-08-630-019A-9/c
; Sequence 9, Application US/08630019A
; Patent No. 6015710
;  GENERAL INFORMATION:
;    APPLICANT:  Shay, Jerry W.
;    APPLICANT:  Wright, Woodring E.
;    APPLICANT:  Piatyszek, Mieczyslaw A.
;    APPLICANT:  Corey, David
;    APPLICANT:  No. 6015710ton, James C.
;    TITLE OF INVENTION:  Modulation of Mammalian Telomerase by
;    TITLE OF INVENTION:  Peptide Nucleic Acids
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
```

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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/630,019A
;      FILING DATE:  09-JUN-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-001600US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "peptide nucleic acid (PNA),
;      DESCRIPTION:  where (deoxy)ribose-phosphate linkages are replaced by
;      DESCRIPTION:  N-(2-aminoethyl)glycine units linked to nucleotide bases via
;      DESCRIPTION:  glycine amino nitrogen through a methylenecarbonyl linker"
US-08-630-019A-9

  Query Match             100.0%;  Score 11;  DB 3;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||
Db         11 CTAACCCTAAC 1


RESULT 10
US-08-630-019A-30
; Sequence 30, Application US/08630019A
; Patent No. 6015710
;  GENERAL INFORMATION:
;    APPLICANT:  Shay, Jerry W.
;    APPLICANT:  Wright, Woodring E.
;    APPLICANT:  Piatyszek, Mieczyslaw A.
;    APPLICANT:  Corey, David
;    APPLICANT:  No. 6015710ton, James C.
;    TITLE OF INVENTION:  Modulation of Mammalian Telomerase by
;    TITLE OF INVENTION:  Peptide Nucleic Acids
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/630,019A
;      FILING DATE:  09-JUN-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-001600US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
US-08-630-019A-30

  Query Match             100.0%;  Score 11;  DB 3;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              |:||||:|||
Db          1 CUAACCCUAAC 11


RESULT 11
US-08-630-019A-39/c
; Sequence 39, Application US/08630019A
; Patent No. 6015710
;  GENERAL INFORMATION:
;    APPLICANT:  Shay, Jerry W.
;    APPLICANT:  Wright, Woodring E.
;    APPLICANT:  Piatyszek, Mieczyslaw A.
;    APPLICANT:  Corey, David
;    APPLICANT:  No. 6015710ton, James C.
;    TITLE OF INVENTION:  Modulation of Mammalian Telomerase by
;    TITLE OF INVENTION:  Peptide Nucleic Acids
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/630,019A
;      FILING DATE:  09-JUN-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-001600US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "phosphorothioate (PS) nucleic acid"
US-08-630-019A-39

  Query Match             100.0%;  Score 11;  DB 3;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||
Db         11 CTAACCCTAAC 1


RESULT 12
US-08-838-545-13/c
; Sequence 13, Application US/08838545
; Patent No. 6046307
```

```
;  GENERAL INFORMATION:
;    APPLICANT:  Shay, Jerry W.
;    APPLICANT:  Wright, Woodring E.
;    APPLICANT:  Piatyszek, Mieczyslaw A.
;    APPLICANT:  Corey, David R.
;    APPLICANT:  No. 6046307ton, James C.
;    TITLE OF INVENTION:  Modulation of Mammalian Telomerase by
;    TITLE OF INVENTION:  Peptide Nucleic Acids
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/838,545
;      FILING DATE:  09-APR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,019
;      FILING DATE:  09-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-001610US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "peptide nucleic acid (PNA),
;      DESCRIPTION:  where (deoxy(ribose-phosphate linkages are replaced by
;      DESCRIPTION:  N-(2-aminoethyl)glycine units linked to nucleotide bases via
;      DESCRIPTION:  glycine amino N through a methylenecarbonyl linker"
US-08-838-545-13

  Query Match             100.0%;  Score 11;  DB 3;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||| 
Db         11 CTAACCCTAAC 1


RESULT 13
US-08-838-545-31
; Sequence 31, Application US/08838545
; Patent No. 6046307
;  GENERAL INFORMATION:
;    APPLICANT:  Shay, Jerry W.
;    APPLICANT:  Wright, Woodring E.
;    APPLICANT:  Piatyszek, Mieczyslaw A.
;    APPLICANT:  Corey, David R.
;    APPLICANT:  No. 6046307ton, James C.
;    TITLE OF INVENTION:  Modulation of Mammalian Telomerase by
;    TITLE OF INVENTION:  Peptide Nucleic Acids
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/838,545
;      FILING DATE:  09-APR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,019
;      FILING DATE:  09-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-001610US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "peptide nucleic acid (PNA),
;      DESCRIPTION:  where (deoxy(ribose-phosphate linkages are replaced by
;      DESCRIPTION:  N-(2-aminoethyl)glycine units linked to nucleotide bases via
;      DESCRIPTION:  glycine amino N through a methylenecarbonyl linker"
US-08-838-545-31

  Query Match             100.0%;  Score 11;  DB 3;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||| 
Db          1 CTAACCCTAAC 11


RESULT 14
US-08-838-545-44/c
; Sequence 44, Application US/08838545
; Patent No. 6046307
;  GENERAL INFORMATION:
;    APPLICANT:  Shay, Jerry W.
;    APPLICANT:  Wright, Woodring E.
;    APPLICANT:  Piatyszek, Mieczyslaw A.
;    APPLICANT:  Corey, David R.
;    APPLICANT:  No. 6046307ton, James C.
;    TITLE OF INVENTION:  Modulation of Mammalian Telomerase by
;    TITLE OF INVENTION:  Peptide Nucleic Acids
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/838,545
;      FILING DATE:  09-APR-1997
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;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,019
;      FILING DATE:  09-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-001610US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "phosphorothioate (PS)
;      DESCRIPTION:  nucleic acid"
US-08-838-545-44

  Query Match             100.0%;  Score 11;  DB 3;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||| |
Db         11 CTAACCCTAAC 1


RESULT 15
US-08-998-443-2
; Sequence 2, Application US/08998443
; Patent No. 6054575
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  Mammalian Telomerase
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/998,443
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/660,678
;      FILING DATE:  05-JUN-1996
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-000811US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
US-08-998-443-2

  Query Match             100.0%;  Score 11;  DB 3;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              |:|||||:|||
Db          1 CUAACCCUAAC 11


Search completed: July  6, 2003, 09:42:20
Job time : 57.9643 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 08:30:00 ; Search time 120.214 Seconds
(without alignments)
142.836 Million cell updates/sec

Title: US-09-540-843-9
Perfect score: 11
Sequence: 1 ctaaccctaac 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 816406

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	11	100.0	11	9	US-09-835-370-63	Sequence 63, Appl
c	2	11	100.0	11	9	US-10-122-630-5	Sequence 5, Appli
	3	11	100.0	11	9	US-10-122-630-9	Sequence 9, Appli
c	4	11	100.0	11	9	US-10-122-633-5	Sequence 5, Appli
	5	11	100.0	11	9	US-10-122-633-9	Sequence 9, Appli
	6	11	100.0	11	10	US-09-057-351-2	Sequence 2, Appli
c	7	11	100.0	13	9	US-09-893-252-4	Sequence 4, Appli
c	8	11	100.0	13	9	US-10-038-335-1	Sequence 1, Appli
c	9	11	100.0	13	9	US-10-038-335-2	Sequence 2, Appli
	10	11	100.0	18	8	US-08-463-404-4	Sequence 4, Appli
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	13	11	100.0	18	9	US-10-132-002-2	Sequence 2, Appli
c	14	11	100.0	18	9	US-10-132-002-4	Sequence 4, Appli
	15	11	100.0	18	9	US-10-238-732-2	Sequence 2, Appli
c	16	11	100.0	18	9	US-10-044-692-295	Sequence 295, App
c	17	11	100.0	18	9	US-10-044-692-296	Sequence 296, App
c	18	11	100.0	18	9	US-10-044-539-295	Sequence 295, App
c	19	11	100.0	18	9	US-10-044-539-296	Sequence 296, App
c	20	11	100.0	18	10	US-09-057-351-26	Sequence 26, Appl
	21	11	100.0	18	10	US-09-947-659-1	Sequence 1, Appli
c	22	11	100.0	18	10	US-09-947-659-2	Sequence 2, Appli
c	23	11	100.0	18	10	US-09-947-659-7	Sequence 7, Appli
c	24	11	100.0	19	10	US-09-817-387-19	Sequence 19, Appl
c	25	11	100.0	20	9	US-09-888-326-808	Sequence 808, App
c	26	11	100.0	20	9	US-10-112-653-824	Sequence 824, App
c	27	11	100.0	20	9	US-10-017-995-853	Sequence 853, App
c	28	11	100.0	20	9	US-09-776-479-853	Sequence 853, App
c	29	11	100.0	20	10	US-09-057-351-40	Sequence 40, Appl
c	30	11	100.0	20	10	US-09-816-248-36	Sequence 36, Appl
c	31	11	100.0	20	10	US-09-816-248-37	Sequence 37, Appl
c	32	11	100.0	21	9	US-10-079-500B-1	Sequence 1, Appli
c	33	11	100.0	21	9	US-10-040-370A-1	Sequence 1, Appli
c	34	11	100.0	21	10	US-09-817-387-23	Sequence 23, Appl
c	35	11	100.0	21	10	US-09-817-387-28	Sequence 28, Appl
	36	11	100.0	21	10	US-09-801-346-2	Sequence 2, Appli
c	37	11	100.0	21	10	US-09-923-541-1	Sequence 1, Appli
c	38	11	100.0	22	9	US-09-940-173A-2	Sequence 2, Appli
c	39	11	100.0	22	9	US-09-940-173A-8	Sequence 8, Appli
c	40	11	100.0	22	9	US-10-109-612-2	Sequence 2, Appli
c	41	11	100.0	22	10	US-09-057-351-41	Sequence 41, Appl
c	42	11	100.0	22	10	US-09-730-893-2	Sequence 2, Appli
c	43	11	100.0	22	10	US-09-730-893-8	Sequence 8, Appli
c	44	11	100.0	23	10	US-09-817-387-14	Sequence 14, Appl
c	45	11	100.0	23	10	US-09-817-387-16	Sequence 16, Appl

ALIGNMENTS

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RESULT 1
US-09-835-370-63/c
; Sequence 63, Application US/09835370
; Publication No. US20030022172A1
; GENERAL INFORMATION:
;  APPLICANT: UHLMANN, EUGEN
;  APPLICANT:  BREIPOHL, GERHARD
;  APPLICANT:  WILL, DAVID W
;  TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND
;  TITLE OF INVENTION:  PROCESSES FOR PREPARING THEM
;  FILE REFERENCE: 02481.1742 SEQUENCE LISTING
;  CURRENT APPLICATION NUMBER: US/09/835,370
;  CURRENT FILING DATE:  2001-04-17
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  nucleotide
;   OTHER INFORMATION: base sequence of PNA derivatives that bind to
;   OTHER INFORMATION: viral and cellular targets
US-09-835-370-63

  Query Match             100.0%;  Score 11;  DB 9;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||| 
Db         11 CTAACCCTAAC 1


RESULT 2
US-10-122-630-5/c
; Sequence 5, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
```

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;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-018
;  CURRENT APPLICATION NUMBER: US/10/122,630
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 08/467,012
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US96/08386
;  PRIOR FILING DATE: 1996-06-03
;  PRIOR APPLICATION NUMBER: US 09/048,927
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-5

  Query Match             100.0%;  Score 11;  DB 9;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||| |
Db         11 CTAACCCTAAC 1


RESULT 3
US-10-122-630-9
; Sequence 9, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-018
;  CURRENT APPLICATION NUMBER: US/10/122,630
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 08/467,012
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US96/08386
;  PRIOR FILING DATE: 1996-06-03
;  PRIOR APPLICATION NUMBER: US 09/048,927
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-9

  Query Match             100.0%;  Score 11;  DB 9;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||| |
Db          1 CTAACCCTAAC 11


RESULT 4
US-10-122-633-5/c
; Sequence 5, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-5

  Query Match             100.0%;  Score 11;  DB 9;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||| |
Db         11 CTAACCCTAAC 1


RESULT 5
US-10-122-633-9
; Sequence 9, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-9

  Query Match             100.0%;  Score 11;  DB 9;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||| |
Db          1 CTAACCCTAAC 11
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RESULT 6
US-09-057-351-2
; Sequence 2, Application US/09057351
; Patent No. US20010034439A1
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  Mammalian Telomerase
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/057,351
;      FILING DATE:  08-APR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/472,802
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-000821US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
US-09-057-351-2

  Query Match             100.0%;  Score 11;  DB 10;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 2.6e+03;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              |:||||:|||
Db          1 CUAACCCUAAC 11


RESULT 7
US-09-893-252-4/c
; Sequence 4, Application US/09893252
; Publication No. US20030012755A1
; GENERAL INFORMATION:
;  APPLICANT: Styczynski, Peter
;  APPLICANT:  Ahluwalia, Gurpreet S.
;  TITLE OF INVENTION: REDUCTION OF HAIR GROWTH
;  FILE REFERENCE: 00216-552001
;  CURRENT APPLICATION NUMBER: US/09/893,252
;  CURRENT FILING DATE:  2001-10-12
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 13
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-893-252-4

  Query Match             100.0%;  Score 11;  DB 9;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||
Db         13 CTAACCCTAAC 3


RESULT 8
US-10-038-335-1/c
; Sequence 1, Application US/10038335
; Publication No. US20030096776A1
; GENERAL INFORMATION:
;  APPLICANT: Ecker, David J.
;  APPLICANT:  Wyatt, Jacqueline
;  APPLICANT:  Bennett, C. Frank
;  APPLICANT:  Hanecak, Ronnie
;  APPLICANT:  Brown-Driver, Vickie
;  APPLICANT:  Vickers, Timothy
;  APPLICANT:  Chiang, Ming-yi
;  APPLICANT:  Anderson, Kevin
;  TITLE OF INVENTION: Modulation Of Telomere Length By Oligonucleotides Having A G-C
;  TITLE OF INVENTION:  Sequence
;  FILE REFERENCE: ISIS-4976
;  CURRENT APPLICATION NUMBER: US/10/038,335
;  CURRENT FILING DATE:  2001-01-02
;  PRIOR APPLICATION NUMBER: 09/299,058
;  PRIOR FILING DATE: 1999-04-23
;  PRIOR APPLICATION NUMBER: 08/403,888
;  PRIOR FILING DATE: 1995-06-12
;  PRIOR APPLICATION NUMBER: PCT/US93/09297
;  PRIOR FILING DATE: 1993-09-29
;  PRIOR APPLICATION NUMBER: 07/954,185
;  PRIOR FILING DATE: 1992-09-29
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: No. US20030096776A1el sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense sequence
US-10-038-335-1

  Query Match             100.0%;  Score 11;  DB 9;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||
Db         13 CTAACCCTAAC 3


RESULT 9
US-10-038-335-2/c
; Sequence 2, Application US/10038335
; Publication No. US20030096776A1
; GENERAL INFORMATION:
;  APPLICANT: Ecker, David J.
;  APPLICANT:  Wyatt, Jacqueline
;  APPLICANT:  Bennett, C. Frank
;  APPLICANT:  Hanecak, Ronnie
;  APPLICANT:  Brown-Driver, Vickie
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;  APPLICANT:  Vickers, Timothy
;  APPLICANT:  Chiang, Ming-yi
;  APPLICANT:  Anderson, Kevin
;  TITLE OF INVENTION: Modulation Of Telomere Length By Oligonucleotides Having A G-Core
;  TITLE OF INVENTION:  Sequence
;  FILE REFERENCE: ISIS-4976
;  CURRENT APPLICATION NUMBER: US/10/038,335
;  CURRENT FILING DATE:  2001-01-02
;  PRIOR APPLICATION NUMBER: 09/299,058
;  PRIOR FILING DATE: 1999-04-23
;  PRIOR APPLICATION NUMBER: 08/403,888
;  PRIOR FILING DATE: 1995-06-12
;  PRIOR APPLICATION NUMBER: PCT/US93/09297
;  PRIOR FILING DATE: 1993-09-29
;  PRIOR APPLICATION NUMBER: 07/954,185
;  PRIOR FILING DATE: 1992-09-29
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: No. US20030096776A1el sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense sequence
US-10-038-335-2

  Query Match             100.0%;  Score 11;  DB 9;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||
Db         13 CTAACCCTAAC 3


RESULT 10
US-08-463-404-4
; Sequence 4, Application US/08463404
; Patent No. US20020127634A1
;  GENERAL INFORMATION:
;    APPLICANT:  Michael D. West
;    APPLICANT:  Jerry W. Shay
;    APPLICANT:  Woodring E. Wright
;    APPLICANT:  Elizabeth Blackburn
;    TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF CONDITIONS
;    TITLE OF INVENTION:  RELATED TO TELOMERE LENGTH AND/OR
;    TITLE OF INVENTION:  TELOMERASE ACTIVITY
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,404
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/060,952
;      FILING DATE:  May 13, 1993
;      APPLICATION NUMBER:  07/882,438
;      FILING DATE:  May 13, 1992
;      APPLICATION NUMBER:  08/038,766
;      FILING DATE:  March 24, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  202/045
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-463-404-4

  Query Match             100.0%;  Score 11;  DB 8;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||
Db          3 CTAACCCTAAC 13


RESULT 11
US-08-463-404-5/c
; Sequence 5, Application US/08463404
; Patent No. US20020127634A1
;  GENERAL INFORMATION:
;    APPLICANT:  Michael D. West
;    APPLICANT:  Jerry W. Shay
;    APPLICANT:  Woodring E. Wright
;    APPLICANT:  Elizabeth Blackburn
;    TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF CONDITIONS
;    TITLE OF INVENTION:  RELATED TO TELOMERE LENGTH AND/OR
;    TITLE OF INVENTION:  TELOMERASE ACTIVITY
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,404
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/060,952
;      FILING DATE:  May 13, 1993
;      APPLICATION NUMBER:  07/882,438
;      FILING DATE:  May 13, 1992
;      APPLICATION NUMBER:  08/038,766
;      FILING DATE:  March 24, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  202/045
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
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;       LENGTH:  18
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-463-404-5

  Query Match             100.0%;  Score 11;  DB 8;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||
Db         16 CTAACCCTAAC 6


RESULT 12
US-09-893-252-1/c
; Sequence 1, Application US/09893252
; Publication No. US20030012755A1
; GENERAL INFORMATION:
;  APPLICANT: Styczynski, Peter
;  APPLICANT:  Ahluwalia, Gurpreet S.
;  TITLE OF INVENTION: REDUCTION OF HAIR GROWTH
;  FILE REFERENCE: 00216-552001
;  CURRENT APPLICATION NUMBER: US/09/893,252
;  CURRENT FILING DATE:  2001-10-12
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-893-252-1

  Query Match             100.0%;  Score 11;  DB 9;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||
Db         16 CTAACCCTAAC 6


RESULT 13
US-10-132-002-2
; Sequence 2, Application US/10132002
; Publication No. US20030022204A1
;   GENERAL INFORMATION:
;        APPLICANT: Lansdorp, Peter
;        TITLE OF INVENTION: Method for Detecting Multiple Copies of
;                            a Repeat Sequence in a Nucleic Acid Molecule
;        NUMBER OF SEQUENCES: 14
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: HOWSON & HOWSON
;             STREET: 321 No. US20030022204A1ristown Road
;             CITY: Spring House
;             STATE: PA
;             COUNTRY: U.S.A.
;             ZIP: 19477
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/132,002
;             FILING DATE: 25-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/730,635
;             FILING DATE: 11-OCT-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Bak, Mary E.
;             REGISTRATION NUMBER: 31,215
;             REFERENCE/DOCKET NUMBER: B&P7USA
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (215) 540-9200
;             TELEFAX: (215) 540-5818
;             TELEX: N/A
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-132-002-2

  Query Match             100.0%;  Score 11;  DB 9;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||
Db          3 CTAACCCTAAC 13


RESULT 14
US-10-132-002-4/c
; Sequence 4, Application US/10132002
; Publication No. US20030022204A1
;   GENERAL INFORMATION:
;        APPLICANT: Lansdorp, Peter
;        TITLE OF INVENTION: Method for Detecting Multiple Copies of
;                            a Repeat Sequence in a Nucleic Acid Molecule
;        NUMBER OF SEQUENCES: 14
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: HOWSON & HOWSON
;             STREET: 321 No. US20030022204A1ristown Road
;             CITY: Spring House
;             STATE: PA
;             COUNTRY: U.S.A.
;             ZIP: 19477
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/132,002
;             FILING DATE: 25-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/730,635
;             FILING DATE: 11-OCT-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Bak, Mary E.
;             REGISTRATION NUMBER: 31,215
;             REFERENCE/DOCKET NUMBER: B&P7USA
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (215) 540-9200
;             TELEFAX: (215) 540-5818
;             TELEX: N/A
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-132-002-4

  Query Match             100.0%;  Score 11;  DB 9;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
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  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||
Db         16 CTAACCCTAAC 6


RESULT 15
US-10-238-732-2
; Sequence 2, Application US/10238732
; Publication No. US20030077635A1
; GENERAL INFORMATION:
;  APPLICANT: DAKO A/S
;  TITLE OF INVENTION: DENDRIMERS AND METHODS FOR THEIR PREPARATION AND USE
;  FILE REFERENCE: P65587US1
;  CURRENT APPLICATION NUMBER: US/10/238,732
;  CURRENT FILING DATE:  2002-09-11
;  PRIOR APPLICATION NUMBER: 09/606,315
;  PRIOR FILING DATE: 2000-06-29
;  PRIOR APPLICATION NUMBER: PA 1999 00934
;  PRIOR FILING DATE: 1999-06-29
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: linker sequence.
US-10-238-732-2

  Query Match            100.0%;  Score 11;  DB 9;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 2.5e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTAACCCTAAC 11
              ||||||||||
Db          6 CTAACCCTAAC 16


Search completed: July  6, 2003, 12:17:04
Job time : 121.214 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 07:52:05 ; Search time 25.8929 Seconds
(without alignments)
59.220 Million cell updates/sec

Title: US-09-540-843-6
Perfect score: 5
Sequence: 1 catac 5

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 558892

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	5	100.0	5	3	US-08-855-372B-20	Sequence 20, Appl
c	2	5	100.0	5	3	US-09-048-927-4	Sequence 4, Appli
c	3	5	100.0	5	4	US-09-498-851-20	Sequence 20, Appl
	4	5	100.0	7	1	US-08-615-170-10	Sequence 10, Appl
	5	5	100.0	7	1	US-08-615-170-12	Sequence 12, Appl
c	6	5	100.0	7	3	US-09-048-927-3	Sequence 3, Appli
c	7	5	100.0	9	2	US-08-583-276-1	Sequence 1, Appli
c	8	5	100.0	9	3	US-08-646-789A-8	Sequence 8, Appli
c	9	5	100.0	9	3	US-08-646-789A-80	Sequence 80, Appl
c	10	5	100.0	9	3	US-09-048-927-1	Sequence 1, Appli
	11	5	100.0	9	4	US-09-319-648-68	Sequence 68, Appl
c	12	5	100.0	10	1	US-08-335-565A-27	Sequence 27, Appl
	13	5	100.0	10	1	US-08-250-951-1	Sequence 1, Appli
	14	5	100.0	10	1	US-08-232-233-1	Sequence 1, Appli
	15	5	100.0	10	1	US-08-222-177A-422	Sequence 422, App
c	16	5	100.0	10	1	US-08-351-748-23	Sequence 23, Appl
c	17	5	100.0	10	1	US-08-351-748-25	Sequence 25, Appl
	18	5	100.0	10	1	US-08-202-927-25	Sequence 25, Appl
c	19	5	100.0	10	1	US-08-430-536A-23	Sequence 23, Appl
c	20	5	100.0	10	1	US-08-430-536A-25	Sequence 25, Appl
c	21	5	100.0	10	1	US-08-171-718-45	Sequence 45, Appl
	22	5	100.0	10	2	US-08-703-601-1	Sequence 1, Appli
c	23	5	100.0	10	2	US-08-684-547-23	Sequence 23, Appl
c	24	5	100.0	10	2	US-08-684-547-25	Sequence 25, Appl
c	25	5	100.0	10	3	US-08-469-318-174	Sequence 174, App
c	26	5	100.0	10	3	US-08-468-609A-174	Sequence 174, App
c	27	5	100.0	10	3	US-08-478-087-45	Sequence 45, Appl
	28	5	100.0	10	3	US-09-063-450-24	Sequence 24, Appl
c	29	5	100.0	10	3	US-09-063-450-33	Sequence 33, Appl
	30	5	100.0	10	4	US-09-123-638-1	Sequence 1, Appli
c	31	5	100.0	10	4	US-08-646-695-30	Sequence 30, Appl
c	32	5	100.0	10	4	US-08-875-533-31	Sequence 31, Appl
c	33	5	100.0	10	4	US-08-446-872A-174	Sequence 174, App
	34	5	100.0	10	4	US-09-724-753-1	Sequence 1, Appli
c	35	5	100.0	10	4	US-08-762-227A-174	Sequence 174, App
	36	5	100.0	10	5	PCT-US92-09827-1	Sequence 1, Appli
c	37	5	100.0	10	5	PCT-US95-01185-174	Sequence 174, App
	38	5	100.0	10	5	PCT-US95-02419-25	Sequence 25, Appl
c	39	5	100.0	10	5	PCT-US96-06053-30	Sequence 30, Appl
	40	5	100.0	10	6	5198343-3	Patent No. 5198343
c	41	5	100.0	11	1	US-08-401-512-19	Sequence 19, Appl
c	42	5	100.0	11	1	US-08-147-696E-4	Sequence 4, Appli
c	43	5	100.0	11	1	US-08-696-139-6	Sequence 6, Appli
c	44	5	100.0	11	1	US-08-484-334-4	Sequence 4, Appli
	45	5	100.0	11	2	US-08-441-887A-82	Sequence 82, Appl

ALIGNMENTS

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RESULT 1
US-08-855-372B-20/c
; Sequence 20, Application US/08855372B
; Patent No. 6090549
;  GENERAL INFORMATION:
;    APPLICANT:  Mirzabekov, Andrei D
;    APPLICANT:  Parinov, Sergei V
;    APPLICANT:  Barsky, Victor E
;    APPLICANT:  Kirillov, Eugene V
;    APPLICANT:  Dubiley, Svetlana A
;    TITLE OF INVENTION:  Use of Continuous/Contiguous Stacking Hybridization as a Di
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHERSKOV & FLAYNIK
;      STREET:  20 N. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.50 inch, 1.4 MB storage
;      COMPUTER:  PC
;      OPERATING SYSTEM:  Microsoft Windows 98
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/855,372B
;      FILING DATE:  13-MAY-97
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.S. 08/587,332
;      FILING DATE:  16-JAN-96
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cherskov, Michael J.
;      REGISTRATION NUMBER:  33,664
;      REFERENCE/DOCKET NUMBER:  ANL-IN-95-027
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 621-1330
;      TELEFAX:  (312) 621-0088
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  No. 6090549 Applicable
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  yes
US-08-855-372B-20

  Query Match           100.0%;  Score 5;  DB 3;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 5.8e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 CATAC 5
              |||||
Db          5 CATAC 1


RESULT 2
US-09-048-927-4/c
; Sequence 4, Application US/09048927
; Patent No. 6147056
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT: Yaar, Mina
;  APPLICANT: Eller, Mark
;  TITLE OF INVENTION: Use of Locally Applied DNA Fragments
;  FILE REFERENCE: BU94-68A2
;  CURRENT APPLICATION NUMBER: US/09/048,927
;  CURRENT FILING DATE: 1998-03-26
;  EARLIER APPLICATION NUMBER: 08/952,697
;  EARLIER FILING DATE: 1996-06-03
;  EARLIER APPLICATION NUMBER: 08/467,012
;  EARLIER FILING DATE: 1995-06-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 5
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA Fragment
US-09-048-927-4

  Query Match             100.0%;  Score 5;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          5 CATAC 1


RESULT 3
US-09-498-851-20/c
; Sequence 20, Application US/09498851
; Patent No. 6440671
;  GENERAL INFORMATION:
;    APPLICANT:  Mirzabekov, Andrei D
;    APPLICANT:  Parinov, Sergei V
;    APPLICANT:  Barsky, Victor E
;    APPLICANT:  Kirillov, Eugene V
;    APPLICANT:  Dubiley, Svetlana A
;    TITLE OF INVENTION:  Use of Continuous/Contiguous
;    TITLE OF INVENTION:  Stacking Hybridization as a Diagnostic Tool.
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHERSKOV & FLAYNIK
;      STREET:  20 N. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.50 inch, 1.4 MB storage
;      COMPUTER:  PC
;      OPERATING SYSTEM:  Microsoft Windows 98
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/498,851
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/855,372
;      FILING DATE:  13-MAY-97
;      APPLICATION NUMBER:  U.S. 08/587,332
;      FILING DATE:  16-JAN-96
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cherskov, Michael J.
;      REGISTRATION NUMBER:  33,664
;      REFERENCE/DOCKET NUMBER:  ANL-IN-95-027
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 621-1330
;      TELEFAX:  (312) 621-0088
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  No. 6440671 Applicable
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  yes
US-09-498-851-20

  Query Match             100.0%;  Score 5;  DB 4;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          5 CATAC 1


RESULT 4
US-08-615-170-10
; Sequence 10, Application US/08615170
; Patent No. 5776776
;  GENERAL INFORMATION:
;    APPLICANT:  ORDAHL, Charles P.
;    APPLICANT:  AZAKIE, Anthony
;    APPLICANT:  MAR, Janet H.
;    APPLICANT:  FARRANCE, Iain K.G.
;    APPLICANT:  HALL, Deborah E.
;    APPLICANT:  STEWART, Alexandre F.R.
;    APPLICANT:  LARKIN, Sarah B.
;    TITLE OF INVENTION:  DTEF-1 ISOFORMS AND USES THEREOF
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  Steuart Street Tower, One Market Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105-1493
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/615,170
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01526
;      FILING DATE:  06-FEB-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/191,493
;      FILING DATE:  04-FEB-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Heslin, James M.
;      REGISTRATION NUMBER:  29,541
;      REFERENCE/DOCKET NUMBER:  2307U-053120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  10:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..7
;      OTHER INFORMATION:  /standard_name= "Sph-II binding
;      OTHER INFORMATION:  site in SV40"
US-08-615-170-10

  Query Match             100.0%;  Score 5;  DB 1;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          1 CATAC 5


RESULT 5
US-08-615-170-12
; Sequence 12, Application US/08615170
; Patent No. 5776776
;  GENERAL INFORMATION:
;    APPLICANT:  ORDAHL, Charles P.
;    APPLICANT:  AZAKIE, Anthony
;    APPLICANT:  MAR, Janet H.
;    APPLICANT:  FARRANCE, Iain K.G.
;    APPLICANT:  HALL, Deborah E.
;    APPLICANT:  STEWART, Alexandre F.R.
;    APPLICANT:  LARKIN, Sarah B.
;    TITLE OF INVENTION:  DTEF-1 ISOFORMS AND USES THEREOF
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  Steuart Street Tower, One Market Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105-1493
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/615,170
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01526
;      FILING DATE:  06-FEB-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/191,493
;      FILING DATE:  04-FEB-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Heslin, James M.
;      REGISTRATION NUMBER:  29,541
;      REFERENCE/DOCKET NUMBER:  2307U-053120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..7
;      OTHER INFORMATION:  /standard_name= "Rat beta-Myosin
;      OTHER INFORMATION:  Heavy Chain M-CAT binding element"
US-08-615-170-12

  Query Match             100.0%;  Score 5;  DB 1;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          1 CATAC 5


RESULT 6
US-09-048-927-3/c
; Sequence 3, Application US/09048927
; Patent No. 6147056
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT: Yaar, Mina
;  APPLICANT: Eller, Mark
;  TITLE OF INVENTION: Use of Locally Applied DNA Fragments
;  FILE REFERENCE: BU94-68A2
;  CURRENT APPLICATION NUMBER: US/09/048,927
;  CURRENT FILING DATE: 1998-03-26
;  EARLIER APPLICATION NUMBER: 08/952,697
;  EARLIER FILING DATE: 1996-06-03
;  EARLIER APPLICATION NUMBER: 08/467,012
;  EARLIER FILING DATE: 1995-06-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA Fragment
US-09-048-927-3

  Query Match             100.0%;  Score 5;  DB 3;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          6 CATAC 2


RESULT 7
US-08-583-276-1/c
; Sequence 1, Application US/08583276
; Patent No. 5837536
;  GENERAL INFORMATION:
;    APPLICANT:  McDonagh, Kevin T.
;    APPLICANT:  Nienhuis, Arthur
;    APPLICANT:  Tolstoshev, Paul
;    TITLE OF INVENTION:  IMPROVED EXPRESSION OF HUMAN
;    TITLE OF INVENTION:  MULTIDRUG RESISTANCE GENES AND IMPROVED
;    TITLE OF INVENTION:  SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;      ADDRESSEE:  Cecchi & Stewart
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
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;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  DW4.V2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/583,276
;      FILING DATE:  05-JAN-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/332,444
;      FILING DATE:  31-OCT-1994
;      APPLICATION NUMBER:  07/887,712
;      FILING DATE:  22-MAY-1992
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  singular
;      TOPOLOGY:  linear
;    MOLECULE TYPE:
;      DESCRIPTION:  Genomic DNA
US-08-583-276-1

  Query Match           100.0%;  Score 5;  DB 2;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          8 CATAC 4


RESULT 8
US-08-646-789A-8/c
; Sequence 8, Application US/08646789A
; Patent No. 6022863
;  GENERAL INFORMATION:
;    APPLICANT:  Peyman, John A.
;    TITLE OF INVENTION:  REGULATION OF GENE EXPRESSION
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PENNIE & EDMONDS
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,789A
;      FILING DATE:  May 21, 1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  6523-006
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-646-789A-8

  Query Match           100.0%;  Score 5;  DB 3;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          5 CATAC 1


RESULT 9
US-08-646-789A-80/c
; Sequence 80, Application US/08646789A
; Patent No. 6022863
;  GENERAL INFORMATION:
;    APPLICANT:  Peyman, John A.
;    TITLE OF INVENTION:  REGULATION OF GENE EXPRESSION
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PENNIE & EDMONDS
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,789A
;      FILING DATE:  May 21, 1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  6523-006
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  80:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
US-08-646-789A-80

  Query Match           100.0%;  Score 5;  DB 3;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          5 CATAC 1


RESULT 10
US-09-048-927-1/c
; Sequence 1, Application US/09048927
; Patent No. 6147056
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT: Yaar, Mina
;  APPLICANT: Eller, Mark
;  TITLE OF INVENTION: Use of Locally Applied DNA Fragments
;  FILE REFERENCE: BU94-68A2
;  CURRENT APPLICATION NUMBER: US/09/048,927
;  CURRENT FILING DATE: 1998-03-26
;  EARLIER APPLICATION NUMBER: 08/952,697
;  EARLIER FILING DATE: 1996-06-03
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;  EARLIER APPLICATION NUMBER: 08/467,012
;  EARLIER FILING DATE: 1995-06-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA Fragment
US-09-048-927-1

  Query Match            100.0%;  Score 5;  DB 3;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          7 CATAC 3


RESULT 11
US-09-319-648-68
; Sequence 68, Application US/09319648
; Patent No. 6451530
;   GENERAL INFORMATION:
;        APPLICANT: Hawkins, Mary
;        TITLE OF INVENTION: Fluorescent Nucleotide Analog Hairpin
;                            Formation for Detection of Nucleic Acid Hybridization
;        NUMBER OF SEQUENCES: 68
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/319,648
;             FILING DATE: 30-Jul-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 60/032,844
;             FILING DATE: 13-DEC-1996
;             APPLICATION NUMBER: WO PCT/US97/22448
;             FILING DATE: 10-DEC-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Fang, Carol
;             REGISTRATION NUMBER: 48,631
;             REFERENCE/DOCKET NUMBER: 015280-288100US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 68:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 9 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-319-648-68

  Query Match            100.0%;  Score 5;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          3 CATAC 7


RESULT 12
US-08-335-565A-27/c
; Sequence 27, Application US/08335565A
; Patent No. 5527671
;  GENERAL INFORMATION:
;    APPLICANT:  Li, Kening
;    APPLICANT:  Rouse, Douglas I.
;    APPLICANT:  German, Thomas L.
;    TITLE OF INVENTION:  ASSAY FOR VERTICILLIUM DAHLIAE
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles and Brady
;      STREET:  1 South Pinckney St., PO BOX 2113
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  USA
;      ZIP:  53701-2113
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/335,565A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27,386
;      REFERENCE/DOCKET NUMBER:  960296.93065
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-335-565A-27

  Query Match            100.0%;  Score 5;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 6.1e+04;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db         10 CATAC 6


RESULT 13
US-08-250-951-1
; Sequence 1, Application US/08250951
; Patent No. 5532129
;  GENERAL INFORMATION:
;    APPLICANT:  Heller, Michael J
;    TITLE OF INVENTION:  SELF-ORGANIZING MOLECULAR PHOTONIC
;    TITLE OF INVENTION:  STRUCTURES BASED ON CHROMOPHORE- AND FLUROPHORE-CONTAINING
;    TITLE OF INVENTION:  POLYNUCLEOTIDES AND METHODS OF THEIR USE
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bingham & Fitting
;      STREET:  12526 High Bluff Drive, Suite 300
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92130
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/250,951
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/790,262
;       FILING DATE:  07-NOV-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Fitting, Thomas
;       REGISTRATION NUMBER:  34,163
;       REFERENCE/DOCKET NUMBER:  HEL0002P
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  619-792-3680
;       TELEFAX:  619-792-8477
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  10
;       OTHER INFORMATION:  /note= "Donor chromophore at the 3'
;       OTHER INFORMATION:  T nucleotide"
US-08-250-951-1

  Query Match             100.0%;  Score 5;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 6.1e+04;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          4 CATAC 8


RESULT 14
US-08-232-233-1
; Sequence 1, Application US/08232233
; Patent No. 5565322
;  GENERAL INFORMATION:
;    APPLICANT:  Michael J. Heller
;    TITLE OF INVENTION:  SELF-ORGANIZING MOLECULAR PHOTONIC
;    TITLE OF INVENTION:  STRUCTURES BASED ON CHROMOPHORE- AND FLUOROPHORE-
;    TITLE OF INVENTION:  CONTAINING POLYNUCLEOTIDES AND METHODS OF THEIR USE
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  611 West Sixth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,233
;      FILING DATE:  May 4, 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/790,262
;      FILING DATE:  No. 5565322ember 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;       NAME:  Murphy, David B.
;       REGISTRATION NUMBER:  31,125
;       REFERENCE/DOCKET NUMBER:  207/170
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  10
;       OTHER INFORMATION:  /note-"Donor chromphore at the 3' T nucleotide"
US-08-232-233-1

  Query Match             100.0%;  Score 5;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 6.1e+04;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          4 CATAC 8


RESULT 15
US-08-222-177A-422
; Sequence 422, Application US/08222177A
; Patent No. 5582979
;  GENERAL INFORMATION:
;    APPLICANT:  Weber, James L.
;    TITLE OF INVENTION:  LENGTH POLYMORPHISMS IN
;    TITLE OF INVENTION:  (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
;    NUMBER OF SEQUENCES:  460
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DeWitt Ross & Stevens, S.C.
;      STREET:  8000 Excelsior Drive, Suite 401
;      CITY:  Madison
;      STATE:  Wisconsin
;      COUNTRY:  USA
;      ZIP:  53717-1914
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/222,177A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/341,562
;      FILING DATE:  21-APR-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sara, Charles S.
;      REGISTRATION NUMBER:  30,492
;      REFERENCE/DOCKET NUMBER:  09865.601
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (608) 831-2100
;      TELEFAX:  (608) 831-2106
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  422:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
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;    MOLECULE TYPE:  DNA (genomic)
US-08-222-177A-422

  Query Match             100.0%;  Score 5;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 6.1e+04;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          4 CATAC 8


Search completed: July 6, 2003, 09:42:19
Job time : 27.8929 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 08:30:00 ; Search time 54.6429 Seconds
(without alignments)
142.836 Million cell updates/sec

Title: US-09-540-843-6
Perfect score: 5
Sequence: 1 catac 5

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 816406

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	5	100.0	5	9	US-10-122-630-4	Sequence 4, Appli
	2	5	100.0	5	9	US-10-122-630-6	Sequence 6, Appli
c	3	5	100.0	5	9	US-10-122-633-4	Sequence 4, Appli
	4	5	100.0	5	9	US-10-122-633-6	Sequence 6, Appli
c	5	5	100.0	7	9	US-10-122-630-3	Sequence 3, Appli
c	6	5	100.0	7	9	US-10-122-630-7	Sequence 7, Appli
c	7	5	100.0	7	9	US-10-122-633-3	Sequence 3, Appli
c	8	5	100.0	7	9	US-10-122-633-7	Sequence 7, Appli
	9	5	100.0	8	10	US-09-142-593-11	Sequence 11, Appl
	10	5	100.0	8	10	US-09-927-886-17	Sequence 17, Appl
	11	5	100.0	8	10	US-09-861-014-6	Sequence 6, Appli
c	12	5	100.0	9	9	US-10-122-630-1	Sequence 1, Appli
c	13	5	100.0	9	9	US-10-122-633-1	Sequence 1, Appli
	14	5	100.0	9	9	US-10-096-596-32	Sequence 32, Appl
	15	5	100.0	9	9	US-09-990-186-623	Sequence 623, App
c	16	5	100.0	9	9	US-09-990-186-2220	Sequence 2220, Ap
c	17	5	100.0	9	9	US-09-990-186-2256	Sequence 2256, Ap
	18	5	100.0	9	9	US-09-989-994-623	Sequence 623, App
c	19	5	100.0	9	9	US-09-989-994-2220	Sequence 2220, Ap
c	20	5	100.0	9	9	US-09-989-994-2256	Sequence 2256, Ap
	21	5	100.0	9	10	US-09-989-789-623	Sequence 623, App
c	22	5	100.0	9	10	US-09-989-789-2220	Sequence 2220, Ap
c	23	5	100.0	9	10	US-09-989-789-2256	Sequence 2256, Ap
c	24	5	100.0	10	9	US-10-006-542B-5	Sequence 5, Appli
	25	5	100.0	10	9	US-09-962-602-7	Sequence 7, Appli
c	26	5	100.0	10	9	US-09-962-602-8	Sequence 8, Appli
	27	5	100.0	10	9	US-09-990-186-622	Sequence 622, App
c	28	5	100.0	10	9	US-09-990-186-636	Sequence 636, App
c	29	5	100.0	10	9	US-09-990-186-1338	Sequence 1338, Ap
c	30	5	100.0	10	9	US-09-990-186-1341	Sequence 1341, Ap
c	31	5	100.0	10	9	US-09-990-186-1342	Sequence 1342, Ap
c	32	5	100.0	10	9	US-09-990-186-1343	Sequence 1343, Ap
	33	5	100.0	10	9	US-09-989-994-622	Sequence 622, App
c	34	5	100.0	10	9	US-09-989-994-636	Sequence 636, App
c	35	5	100.0	10	9	US-09-989-994-1338	Sequence 1338, Ap
c	36	5	100.0	10	9	US-09-989-994-1341	Sequence 1341, Ap
c	37	5	100.0	10	9	US-09-989-994-1342	Sequence 1342, Ap
c	38	5	100.0	10	9	US-09-989-994-1343	Sequence 1343, Ap
	39	5	100.0	10	10	US-09-822-250-16	Sequence 16, Appl
c	40	5	100.0	10	10	US-09-398-399-31	Sequence 31, Appl
	41	5	100.0	10	10	US-09-989-789-622	Sequence 622, App
c	42	5	100.0	10	10	US-09-989-789-636	Sequence 636, App
c	43	5	100.0	10	10	US-09-989-789-1338	Sequence 1338, Ap
c	44	5	100.0	10	10	US-09-989-789-1341	Sequence 1341, Ap
c	45	5	100.0	10	10	US-09-989-789-1342	Sequence 1342, Ap

ALIGNMENTS

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RESULT 1
US-10-122-630-4/c
; Sequence 4, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-018
;  CURRENT APPLICATION NUMBER: US/10/122,630
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 08/467,012
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US96/08386
;  PRIOR FILING DATE: 1996-06-03
;  PRIOR APPLICATION NUMBER: US 09/048,927
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 5
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-4

  Query Match             100.0%;  Score 5;  DB 9;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          5 CATAC 1
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RESULT 2
US-10-122-630-6
; Sequence 6, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-018
;  CURRENT APPLICATION NUMBER: US/10/122,630
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 08/467,012
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US96/08386
;  PRIOR FILING DATE: 1996-06-03
;  PRIOR APPLICATION NUMBER: US 09/048,927
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 5
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-6

  Query Match           100.0%;  Score 5;  DB 9;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 3e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          1 CATAC 5


RESULT 3
US-10-122-633-4/c
; Sequence 4, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 5
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-4

  Query Match           100.0%;  Score 5;  DB 9;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 3e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          5 CATAC 1


RESULT 4
US-10-122-633-6
; Sequence 6, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 5
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-6

  Query Match           100.0%;  Score 5;  DB 9;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 3e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          1 CATAC 5


RESULT 5
US-10-122-630-3/c
; Sequence 3, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-018
;  CURRENT APPLICATION NUMBER: US/10/122,630
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 08/467,012
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US96/08386
;  PRIOR FILING DATE: 1996-06-03
;  PRIOR APPLICATION NUMBER: US 09/048,927
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-3
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  Query Match           100.0%;  Score 5;  DB 9;  Length 7;
  Best Local Similarity  100.0%;  Pred. No. 2.2e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          6 CATAC 2


RESULT 6
US-10-122-630-7/c
; Sequence 7, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-018
;  CURRENT APPLICATION NUMBER: US/10/122,630
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 08/467,012
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US96/08386
;  PRIOR FILING DATE: 1996-06-03
;  PRIOR APPLICATION NUMBER: US 09/048,927
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-7

  Query Match           100.0%;  Score 5;  DB 9;  Length 7;
  Best Local Similarity  100.0%;  Pred. No. 2.2e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          6 CATAC 2


RESULT 7
US-10-122-633-3/c
; Sequence 3, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-3

  Query Match           100.0%;  Score 5;  DB 9;  Length 7;
  Best Local Similarity  100.0%;  Pred. No. 2.2e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          6 CATAC 2


RESULT 8
US-10-122-633-7/c
; Sequence 7, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-7

  Query Match           100.0%;  Score 5;  DB 9;  Length 7;
  Best Local Similarity  100.0%;  Pred. No. 2.2e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          6 CATAC 2


RESULT 9
US-09-142-593-11
; Sequence 11, Application US/09142593
; Patent No. US20020016975A1
;  GENERAL INFORMATION:
;    APPLICANT:  HACKETT ET AL.
;    TITLE OF INVENTION:  DNA-BASED TRANSPOSON SYSTEM FOR THE
;    TITLE OF INVENTION:  INTRODUCTION OF NUCLEIC ACID INTO DNA OF A CELL
;    NUMBER OF SEQUENCES:  63
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MUETING, RAASCH & GEBHARDT, P.A.
;      STREET:  119 NORTH FOURTH STREET, SUITE 203
;      CITY:  MINNEAPOLIS
;      STATE:  MINNESOTA
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
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;      APPLICATION NUMBER:  US/09/142,593
;      FILING DATE:  10-SEP-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/040,664
;      FILING DATE:  11-MAR-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/053,868
;      FILING DATE:  28-JUL-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/065,303
;      FILING DATE:  13-NOV-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US98/04687
;      FILING DATE:  11-MAR-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SANDBERG, VICTORIA A.
;      REGISTRATION NUMBER:  41,287
;      REFERENCE/DOCKET NUMBER:  110.00450101
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-305-1226
;      TELEFAX:  612-305-1228
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-142-593-11

  Query Match            100.0%;  Score 5;  DB 10;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          2 CATAC 6


RESULT 10
US-09-927-886-17
; Sequence 17, Application US/09927886
; Patent No. US20020103152A1
; GENERAL INFORMATION:
;  APPLICANT: Kay, Mark A.
;  APPLICANT:  Yant, Stephen
;  TITLE OF INVENTION: Methods of In Vivo Gene Transfer Using a
;  TITLE OF INVENTION:  Sleeping Beauty Transposon System
;  FILE REFERENCE: STAN-160CIP
;  CURRENT APPLICATION NUMBER: US/09/927,886
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: 60/162,279
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: 09/440,301
;  PRIOR FILING DATE: 1999-11-17
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: transposon repeat sequence
US-09-927-886-17

  Query Match            100.0%;  Score 5;  DB 10;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          2 CATAC 6


RESULT 11
US-09-861-014-6
; Sequence 6, Application US/09861014
; Patent No. US20020115216A1
; GENERAL INFORMATION:
;  APPLICANT: Steer, Clifford
;  APPLICANT:  Kren, Betsy
;  APPLICANT:  Linehan-Stieers, Cheryle
;  APPLICANT:  McIvor, R.
;  APPLICANT:  Hackett, Perry
;  TITLE OF INVENTION: Composition for Delivery of Compounds to Cells
;  FILE REFERENCE: 110.01330101
;  CURRENT APPLICATION NUMBER: US/09/861,014
;  CURRENT FILING DATE:  2001-05-19
;  PRIOR APPLICATION NUMBER: US 60/206,002
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 60/285,121
;  PRIOR FILING DATE: 2001-04-20
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Direct repeat sequence
US-09-861-014-6

  Query Match            100.0%;  Score 5;  DB 10;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          2 CATAC 6


RESULT 12
US-10-122-630-1/c
; Sequence 1, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-018
;  CURRENT APPLICATION NUMBER: US/10/122,630
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 08/467,012
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US96/08386
;  PRIOR FILING DATE: 1996-06-03
;  PRIOR APPLICATION NUMBER: US 09/048,927
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-1

  Query Match            100.0%;  Score 5;  DB 9;  Length 9;
```

```
  Best Local Similarity   100.0%;  Pred. No. 1.7e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          7 CATAC 3


RESULT 13
US-10-122-633-1/c
; Sequence 1, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-1

  Query Match             100.0%;  Score 5;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          7 CATAC 3


RESULT 14
US-10-096-596-32
; Sequence 32, Application US/10096596
; Publication No. US20030049653A1
; GENERAL INFORMATION:
;  APPLICANT: Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  APPLICANT:  Velculescu, Victor
;  APPLICANT:  Zhang, Lin
;  TITLE OF INVENTION: METHOD FOR SERIAL ANLAYSIS OF GENE EXPRESSION
;  FILE REFERENCE: 001107.00242
;  CURRENT APPLICATION NUMBER: US/10/096,596
;  CURRENT FILING DATE:  2002-03-14
;  PRIOR APPLICATION NUMBER: US 08/527,154
;  PRIOR FILING DATE: 1995-09-12
;  PRIOR APPLICATION NUMBER: US 08/544,861
;  PRIOR FILING DATE: 1995-10-18
;  PRIOR APPLICATION NUMBER: US 09/107,228
;  PRIOR FILING DATE: 1998-06-30
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-096-596-32

  Query Match             100.0%;  Score 5;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          3 CATAC 7


RESULT 15
US-09-990-186-623
; Sequence 623, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 623
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-623

  Query Match             100.0%;  Score 5;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          2 CATAC 6


Search completed: July  6, 2003, 12:17:03
Job time : 55.6429 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 07:33:45 ; Search time 745.536 Seconds
(without alignments)
108.616 Million cell updates/sec

Title: US-09-540-843-6
Perfect score: 5
Sequence: 1 catac 5

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 60474

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	5	100.0	14	13	BM398220	BM398220 5009-0-42
	2	5	100.0	16	9	AI424037	AI424037 tf51h06.x
	3	5	100.0	16	9	AI685758	AI685758 tu37g09.x
	4	5	100.0	16	9	AI721735	AI721735 fc31g08.x
	5	5	100.0	16	13	BG928185	BG928185 HNC65-1-D
	6	5	100.0	17	13	BG929060	BG929060 HNC11-1-G
	7	5	100.0	17	14	C21103	C21103 HUMGS000262
	8	5	100.0	18	13	BM397954	BM397954 5009-0-39
c	9	5	100.0	19	9	AA977115	AA977115 oq24c08.s
	10	5	100.0	19	9	AI120725	AI120725 ub72b11.r
c	11	5	100.0	19	9	AI747751	AI747751 ul21h05.x
c	12	5	100.0	19	14	C00646	C00646 HUMGS000819
c	13	5	100.0	19	17	AZ341880	AZ341880 1M0074O04
	14	5	100.0	19	17	AZ345849	AZ345849 1M0080D16
	15	5	100.0	19	17	AZ355195	AZ355195 1M0094G22
	16	5	100.0	19	17	AZ406137	AZ406137 1M0175F16
c	17	5	100.0	19	17	AZ422163	AZ422163 1M0200B22
c	18	5	100.0	19	17	AZ434551	AZ434551 1M0221C12
	19	5	100.0	19	17	AZ464990	AZ464990 1M0274G11
	20	5	100.0	19	17	AZ486152	AZ486152 1M0314A04
c	21	5	100.0	19	17	AZ579566	AZ579566 1M0367L08
	22	5	100.0	19	17	AZ614702	AZ614702 1M0443F10
	23	5	100.0	19	17	AZ626685	AZ626685 1M0467M01
c	24	5	100.0	19	17	AZ645469	AZ645469 1M0510L24
c	25	5	100.0	19	17	AZ647364	AZ647364 1M0513O16
c	26	5	100.0	19	17	AZ759906	AZ759906 1M0553C10
c	27	5	100.0	19	17	AZ766086	AZ766086 1M0563G19
	28	5	100.0	19	17	AZ799396	AZ799396 2M0056N18
	29	5	100.0	19	17	AZ815067	AZ815067 2M0083P01
c	30	5	100.0	19	17	AZ817238	AZ817238 2M0086E01
	31	5	100.0	19	17	AZ839614	AZ839614 2M0135N16
	32	5	100.0	19	17	AZ864822	AZ864822 2M0174C08
	33	5	100.0	19	17	AZ942806	AZ942806 2M0203F09
	34	5	100.0	19	17	AZ948421	AZ948421 2M0211A01
c	35	5	100.0	19	17	AZ949895	AZ949895 2M0213N08
c	36	5	100.0	19	17	AZ953217	AZ953217 2M0218A23
	37	5	100.0	19	17	AZ987324	AZ987324 2M0269B21
	38	5	100.0	19	17	AZ990856	AZ990856 2M0274F14
	39	5	100.0	20	17	AZ336039	AZ336039 1M0066E09
	40	5	100.0	20	17	AZ359199	AZ359199 1M0101M19
	41	5	100.0	20	17	AZ369273	AZ369273 1M0119H13
c	42	5	100.0	20	17	AZ387347	AZ387347 1M0146K12
c	43	5	100.0	20	17	AZ391065	AZ391065 1M0152H20
c	44	5	100.0	20	17	AZ398474	AZ398474 1M0163G20
	45	5	100.0	20	17	AZ406839	AZ406839 1M0176C16

ALIGNMENTS

RESULT 1
BM398220
LOCUS BM398220 14 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-42-D11.t.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM398220
VERSION BM398220.1 GI:18198273
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 14)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .14
/organism="Tetrahymena thermophila"
/strain="CU428.1"

```
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT        4 a      5 c      0 g      5 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 13;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          1 CATAC 5


RESULT 2
AI424037
LOCUS       AI424037                 16 bp    mRNA    linear   EST 09-MAR-1999
DEFINITION  tf51h06.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2102843 3'
            similar to TR:Q69566 Q69566 ;, mRNA sequence.
ACCESSION   AI424037
VERSION     AI424037.1  GI:4269968
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGAP), Tumor Gene Index
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2102843"
                     /clone_lib="NCI_CGAP_Brn23"
                     /tissue_type="glioblastoma (pooled)"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATATCTTTTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     Library is normalized, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT        8 a      6 c      1 g      1 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 9;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          2 CATAC 6


RESULT 3
AI685758
LOCUS       AI685758                 16 bp    mRNA    linear   EST 27-MAY-1999
DEFINITION  tu37g09.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253280 3'
            similar to TR:Q02393 Q02393 HUMAN PAPILLOMAVIRUS 18 E5 CENTRAL
            SEQUENCE MOTIF PROTEIN 1 ;contains element LTR4 repetitive element
            ;, mRNA sequence.
ACCESSION   AI685758
VERSION     AI685758.1  GI:4897052
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2253280"
                     /clone_lib="NCI_CGAP_Pr28"
                     /sex="male"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; Plasmid DNA from the
                     normalized library NCI_CGAP_Pr22 was prepared, and ss
                     circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     985608-986759, 1101192-1101959, and 1217928-1220615).
                     Subtraction by Bento Soares and M. Fatima Bonaldo.  "
BASE COUNT        7 a      7 c      1 g      1 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 9;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          5 CATAC 9


RESULT 4
AI721735
LOCUS       AI721735                 16 bp    mRNA    linear   EST 07-JUN-2001
DEFINITION  fc31g08.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone
```

```
            IMAGE:3723038 3' similar to SW:YM14_PARTE P15615 HYPOTHETICAL 47.2
            KD PROTEIN ;, mRNA sequence.
ACCESSION   AI721735
VERSION     AI721735.1  GI:5040064
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
            ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
            ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
            Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
            Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
            and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Other_ESTs: fc31g08.y1
            Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: T7 ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="Danio rerio"
                      /db_xref="taxon:7955"
                      /clone="IMAGE:3723038"
                      /clone_lib="Zebrafish WashU MPIMG EST"
                      /sex="mixed"
                      /tissue_type="26 somite embryos, adult livers, shield
                      stage embryos"
                      /lab_host="XL1-blue MRF"
                      /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st
                      strand cDNA was primed with a Not I - oligo(dT)15 primer
                      [5'pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT3'];
                      double-stranded cDNA was ligated to Sal I adaptors (BRL),
                      digested with Not I and cloned into the Not I and Sal I
                      sites of the pSPORT1 vector (BRL). Library was constructed
                      by Matthew Clark (Lehrach lab; ICRF, London and Max Planck
                      Institut fuer Molekulare Genetik,Berlin). cDNAs for EST
                      analysis were selected following oligonucleotide
                      hybridization fingerprinting of arrayed clones from
                      zebrafish late somitogenesis (26 ss), adult liver or
                      embryonic shield stage (5.6 h) libraries.  Fingerprint
                      data were used to computationally cluster cDNAs, and a
                      single cDNA from each cluster was chosen for sequencing.
                      In some cases multiple members of the same cluster were
                      sequenced to assess clustering parameters or single clones
                      were sequenced additional times to assess quality
                      control."
BASE COUNT        6 a      8 c      1 g      1 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 9;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          9 CATAC 13


RESULT 5
BG928185
LOCUS       BG928185                 16 bp    mRNA    linear   EST 06-NOV-2001
DEFINITION  HNC65-1-D12.R.R HNC (Human Normal Cartilage) Homo sapiens cDNA,
            mRNA sequence.
ACCESSION   BG928185
VERSION     BG928185.1  GI:14322708
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
            Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
            Lark,M.W.
  TITLE     Identification and initial characterization of 5000 expressed
            sequenced tags (ESTs) each from adult human normal and
            osteoarthritic cartilage cDNA libraries
  JOURNAL   Osteoarthr. Cartil. 9 (7), 641-653 (2001)
  MEDLINE   21482651
COMMENT     Contact: Sanjay Kumar
            UW2109
            GlaxoSmithKline
            709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
            Tel: 610-270-7245
            Fax: 610-270-5598
            Email: sanjay_kumar-1@gsk.com
            Seq primer: T7.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone_lib="HNC (Human Normal Cartilage)"
                      /tissue_type="cartilage"
                      /lab_host="E.coli DH10 B"
                      /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
                      Directional"
BASE COUNT        4 a      6 c      2 g      3 t      1 others
ORIGIN

  Query Match             100.0%;  Score 5;  DB 13;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          8 CATAC 12


RESULT 6
BG929060
LOCUS       BG929060                 17 bp    mRNA    linear   EST 06-NOV-2001
DEFINITION  HNC11-1-G8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   BG929060
VERSION     BG929060.1  GI:14323583
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
            Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
            Lark,M.W.
  TITLE     Identification and initial characterization of 5000 expressed
            sequenced tags (ESTs) each from adult human normal and
```

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            osteoarthritic cartilage cDNA libraries
  JOURNAL   Osteoarthr. Cartil. 9 (7), 641-653 (2001)
  MEDLINE   21482651
COMMENT     Contact: Sanjay Kumar
            UW2109
            GlaxoSmithKline
            709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
            Tel: 610-270-7245
            Fax: 610-270-5598
            Email: sanjay_kumar-1@gsk.com
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="HNC (Human Normal Cartilage)"
                     /tissue_type="cartilage"
                     /lab_host="E.coli DH10 B"
                     /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
                     Directional"
BASE COUNT        5 a      8 c      2 g      2 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 13;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          6 CATAC 10


RESULT 7
C21103
LOCUS       C21103                   17 bp    mRNA    linear   EST 23-OCT-1996
DEFINITION  HUMGS0002626 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA
            sequence.
ACCESSION   C21103
VERSION     C21103.1  GI:1622213
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Okubo,K.
  TITLE     BodyMap; human gene expression database
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Okubo,K.
            Institute for Molecular and Cellular Biol
            Osaka University
            1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
            Tel: 06-877-5111(ex.3315)
            Email: kousaku@imcb.osaka-u.ac.jp
            Human Gene Signature, 3'-directed cDNA sequence. We are not
            submitting the same cDNA sequence redundantly to DDBJ since 1993.
            For the abundance information of clones with this sequence in this
            library and as well as in other 3'-directed libraries, see '
            http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones
            represented by this GS sequences is also found there.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Human adult (K.Okubo)"
                     /dev_stage="adult"
                     /note="Organ: blood; Vector: l-gt-11; Site_1: Eco-RI;
                     Monocytes were prepared from blood by ficoll-hypaque,
                     percoll  and T cell rosetting purification steps (purity:
                     96 %). mRNA was prepared from  activated monocytes from a
                     patient with rheumatoid arthritis. mRNA was reverse
                     transcribed with MuLV. Using Eco-RI linkers cDNA was
                     cloned into l-gt-11  vector arms. The cDNA library was
                     screened by differential hybidization  using radioactively
                     marked ss-cDNA from activated and non-activated
                     monocytes.  "
BASE COUNT        5 a      5 c      2 g      5 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 14;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          9 CATAC 13


RESULT 8
BM397954
LOCUS       BM397954                 18 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-39-G08.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM397954
VERSION     BM397954.1  GI:18198022
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila.
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
            ,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Tetrahymena thermophila"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT        3 a      7 c      5 g      3 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 13;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          1 CATAC 5


RESULT 9
AA977115/c
LOCUS       AA977115                 19 bp    mRNA    linear   EST 26-MAY-1998
DEFINITION  oq24c08.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1587278 3'
            similar to TR:Q69566 Q69566 ;, mRNA sequence.
ACCESSION   AA977115
VERSION     AA977115.1  GI:3154561
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1  (bases 1 to 19)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1587278"
                     /clone_lib="NCI_CGAP_GC4"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from 3 pooled
                     germ cell tumors, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector.  Library is normalized. Library was constructed by
                     Bento Soares and M. Fatima Bonaldo. "
BASE COUNT        2 a      0 c      7 g     10 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 9;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db         13 CATAC 9


RESULT 10
AI120725
LOCUS       AI120725                 19 bp    mRNA    linear   EST 02-SEP-1998
DEFINITION  ub72b11.r1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
            IMAGE:1383261 5' similar to TR:Q15009 Q15009 ORF, COMPLETE CDS. ;,
            mRNA sequence.
ACCESSION   AI120725
VERSION     AI120725.1  GI:3521049
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:905729
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1383261"
                     /clone_lib="Soares_mammary_gland_NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT        9 a      3 c      4 g      3 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 9;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          7 CATAC 11


RESULT 11
AI747751/c
LOCUS       AI747751                 19 bp    mRNA    linear   EST 22-JUN-1999
DEFINITION  ul21h05.x1 Sugano mouse embryo mewa Mus musculus cDNA clone
            IMAGE:2088249 3' similar to TR:P79101 P79101 CLEAVAGE AND
            POLYADENYLATION SPECIFITY FACTOR PROTEIN. ;, mRNA sequence.
ACCESSION   AI747751
VERSION     AI747751.1  GI:5126015
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
            ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
            ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:995933
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: custom primer used
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
```

```
     source          1. .19
                     /organism="Mus musculus"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:2088249"
                     /clone_lib="Sugano mouse embryo mewa"
                     /dev_stage="embryo, 14 dpc"
                     /lab_host="DH10B"
                     /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
                     Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
                     with an oligo(dT) primer  [ATGTGGCCTTTTTTTTTTTTTTTT];
                     double-stranded cDNA was ligated to a  DraIII adaptor
                     [TGTTGGCCTACTGG], digested and cloned into distinct DraIII
                     sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
                     CACCATGTG). XhoI should be used to isolate the cDNA
                     insert.  Size selection was performed to exclude fragments
                     <1.5kb.  Library constructed by Dr. Sumio Sugano
                     (University of Tokyo Institute of Medical Science).
                     Custom primers  for sequencing: 5' end primer
                     CTTCTGCTCTAAAAGCTGCG and 3' end primer
                     CGACCTGCAGCTCGAGCACA."
BASE COUNT        6 a      2 c      8 g      3 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 9;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db         17 CATAC 13


RESULT 12
C00646/c
LOCUS       C00646                   19 bp    mRNA    linear   EST 23-JUL-1996
DEFINITION  HUMGS0008192 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   C00646
VERSION     C00646.1  GI:1432876
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Okubo,K.
  TITLE     BodyMap; human gene expression database
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Okubo,K.
            Institute for Molecular and Cellular Biol
            Osaka University
            1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
            Tel: 06-877-5111(ex.3315)
            Email: kousaku@imcb.osaka-u.ac.jp
            Human Gene Signature, 3'-directed cDNA sequence. We are not
            submitting the same cDNA sequence redundantly to DDBJ since 1993.
            For the abundance information of clones with this sequence in this
            library and as well as in other 3'-directed libraries, see '
            http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones
            represented by this GS sequences is also found there.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Human adult (K.Okubo)"
                     /dev_stage="adult"
                     /note="Organ: blood; Vector: l-gt-11; Site_1: Eco-RI;
                     Monocytes were prepared from blood by ficoll-hypaque,
                     percoll  and T cell rosetting purification steps (purity:
                     96 %). mRNA was prepared from  activated monocytes from a
                     patient with rheumatoid arthritis. mRNA was reverse
                     transcribed with MuLV. Using Eco-RI linkers cDNA was
                     cloned into l-gt-11  vector arms. The cDNA library was
                     screened by differential hybidization  using radioactively
                     marked ss-cDNA from activated and non-activated
                     monocytes.    "
BASE COUNT        4 a      1 c      8 g      6 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 14;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db         18 CATAC 14


RESULT 13
AZ341880/c
LOCUS       AZ341880                 19 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0074O04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0074O04 R, DNA sequence.
ACCESSION   AZ341880
VERSION     AZ341880.1  GI:10418570
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0074  row: O  column: 04
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0074O04"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
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purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 4 a 4 c 6 g 5 t
ORIGIN

Query Match 100.0%; Score 5; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
|||||
Db 12 CATAC 8

RESULT 14
AZ345849
LOCUS AZ345849 19 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0080D16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080D16 R, DNA sequence.
ACCESSION AZ345849
VERSION AZ345849.1 GI:10425086
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: D column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
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/db_xref="taxon:10090"
/clone="UUGC1M0080D16"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 9 a 4 c 0 g 6 t
ORIGIN

Query Match 100.0%; Score 5; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
|||||
Db 1 CATAC 5

RESULT 15
AZ355195
LOCUS AZ355195 19 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0094G22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0094G22 R, DNA sequence.
ACCESSION AZ355195
VERSION AZ355195.1 GI:10467355
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0094 row: G column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0094G22"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 7 c 3 g 2 t
ORIGIN

Query Match 100.0%; Score 5; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CATAC 5
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Db          8 CATAC 12
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Search completed: July 6, 2003, 09:39:42
Job time : 750.536 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 06:42:31 ; Search time 237.5 Seconds
(without alignments)
612.691 Million cell updates/sec

Title: US-09-540-843-6
Perfect score: 5
Sequence: 1 catac 5

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 774614

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
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13: gb_un:*
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27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
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37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	5	100.0	5	6	AX268756	AX268756 Sequence
2	5	100.0	5	6	AX268758	AX268758 Sequence
c 3	5	100.0	7	6	AX268755	AX268755 Sequence
c 4	5	100.0	7	6	AX268759	AX268759 Sequence
5	5	100.0	8	6	AX047565	AX047565 Sequence
c 6	5	100.0	8	6	AX104946	AX104946 Sequence
c 7	5	100.0	8	6	AX119567	AX119567 Sequence
c 8	5	100.0	9	6	AX268753	AX268753 Sequence
c 9	5	100.0	9	9	S50583	S50583 type I proc
c 10	5	100.0	9	9	S50585	S50585 type I proc
c 11	5	100.0	10	6	A18263	A18263 oligonucleo
12	5	100.0	10	6	AR065157	AR065157 Sequence
c 13	5	100.0	10	6	AR079101	AR079101 Sequence
c 14	5	100.0	10	6	AR079103	AR079103 Sequence
c 15	5	100.0	10	6	AR098909	AR098909 Sequence
16	5	100.0	10	6	AR107335	AR107335 Sequence
c 17	5	100.0	10	6	AR107344	AR107344 Sequence
c 18	5	100.0	10	6	AR123039	AR123039 Sequence
19	5	100.0	10	6	AR136787	AR136787 Sequence
c 20	5	100.0	10	6	AR160130	AR160130 Sequence
c 21	5	100.0	10	6	AR202278	AR202278 Sequence
c 22	5	100.0	10	6	AX080424	AX080424 Sequence
c 23	5	100.0	10	6	AX104930	AX104930 Sequence
c 24	5	100.0	10	6	AX112988	AX112988 Sequence
25	5	100.0	10	6	AX112993	AX112993 Sequence
26	5	100.0	10	6	AX113002	AX113002 Sequence
c 27	5	100.0	10	6	AX152720	AX152720 Sequence
c 28	5	100.0	10	6	AX152760	AX152760 Sequence
c 29	5	100.0	10	6	AX152761	AX152761 Sequence
30	5	100.0	10	6	AX153151	AX153151 Sequence
c 31	5	100.0	10	6	AX153528	AX153528 Sequence
32	5	100.0	10	6	AX153564	AX153564 Sequence
33	5	100.0	10	6	AX153578	AX153578 Sequence
34	5	100.0	10	6	AX153616	AX153616 Sequence
c 35	5	100.0	10	6	AX252791	AX252791 Sequence
c 36	5	100.0	10	6	AX252792	AX252792 Sequence
37	5	100.0	10	6	AX252795	AX252795 Sequence
38	5	100.0	10	6	AX252796	AX252796 Sequence
c 39	5	100.0	10	6	AX252827	AX252827 Sequence
c 40	5	100.0	10	6	AX252828	AX252828 Sequence
41	5	100.0	10	6	AX252832	AX252832 Sequence
c 42	5	100.0	10	6	AX252867	AX252867 Sequence
c 43	5	100.0	10	6	AX252869	AX252869 Sequence
44	5	100.0	10	6	AX252871	AX252871 Sequence
45	5	100.0	10	6	AX252873	AX252873 Sequence

ALIGNMENTS

RESULT 1
AX268756/c
LOCUS AX268756 5 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 4 from Patent WO0174342.
ACCESSION AX268756
VERSION AX268756.1 GI:16541828
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Gilchrest,B.A., Yaar,M. and Eller,M.
TITLE Use of locally applied dna fragments
JOURNAL Patent: WO 0174342-A 4 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)

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                     /note="Synthetic DNA Fragment"
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ORIGIN

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Db          5 CATAC 1


RESULT 2
AX268758
LOCUS       AX268758                  5 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 6 from Patent WO0174342.
ACCESSION   AX268758
VERSION     AX268758.1  GI:16541830
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gilchrest,B.A., Yaar,M. and Eller,M.
  TITLE     Use of locally applied dna fragments
  JOURNAL   Patent: WO 0174342-A 6 11-OCT-2001;
            TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .5
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA Fragment"
BASE COUNT        2 a      2 c      0 g      1 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 5.8e+09;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          1 CATAC 5


RESULT 3
AX268755/c
LOCUS       AX268755                  7 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 3 from Patent WO0174342.
ACCESSION   AX268755
VERSION     AX268755.1  GI:16541827
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gilchrest,B.A., Yaar,M. and Eller,M.
  TITLE     Use of locally applied dna fragments
  JOURNAL   Patent: WO 0174342-A 3 11-OCT-2001;
            TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .7
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA Fragment"
BASE COUNT        3 a      0 c      2 g      2 t
ORIGIN

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  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          6 CATAC 2


RESULT 4
AX268759/c
LOCUS       AX268759                  7 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 7 from Patent WO0174342.
ACCESSION   AX268759
VERSION     AX268759.1  GI:16541831
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gilchrest,B.A., Yaar,M. and Eller,M.
  TITLE     Use of locally applied dna fragments
  JOURNAL   Patent: WO 0174342-A 7 11-OCT-2001;
            TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA Fragment"
BASE COUNT        3 a      0 c      2 g      2 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 6;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+09;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          6 CATAC 2


RESULT 5
AX047565
LOCUS       AX047565                  8 bp    DNA     linear   PAT 15-DEC-2000
DEFINITION  Sequence 6 from Patent WO0068399.
ACCESSION   AX047565
VERSION     AX047565.1  GI:11876656
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Mcivor,R.S., Hackett,P.B. and Aguilar-Cordova,E.
  TITLE     Vector-mediated delivery of integrating transposon sequences
  JOURNAL   Patent: WO 0068399-A 6 16-NOV-2000;
            REGENTS OF THE UNIVERSITY OF MINNESOTA (US) ; BAYLOR COLLEGE OF
            MEDICINE (US) ; McIvor, R. Scott (US) ; Hackett, Perry B. (US) ;
            Aguilar-Cordova, Estuardo (US)
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Direct Repeat Sequence"
BASE COUNT        4 a      3 c      0 g      1 t
ORIGIN

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Qy          1 CATAC 5
              |||||
Db          2 CATAC 6
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RESULT 6
AX104946/c
LOCUS       AX104946                  8 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 1138 from Patent WO0122972.
ACCESSION   AX104946
VERSION     AX104946.1  GI:13921143
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 1138 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .8
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                     /db_xref="taxon:32630"
BASE COUNT        2 a      1 c      2 g      3 t
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  Best Local Similarity  100.0%;  Pred. No. 3.6e+09;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          7 CATAC 3


RESULT 7
AX119567/c
LOCUS       AX119567                  8 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 224 from Patent WO0129251.
ACCESSION   AX119567
VERSION     AX119567.1  GI:14036486
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Messiaen,L. and Callens,T.
  TITLE     Improved mutation analysis of the nf1 gene
  JOURNAL   Patent: WO 0129251-A 224 26-APR-2001;
            UNIVERSITEIT GENT (BE)
FEATURES             Location/Qualifiers
     source          1. .8
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                     /db_xref="taxon:9606"
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Qy          1 CATAC 5
              |||||
Db          7 CATAC 3


RESULT 8
AX268753/c
LOCUS       AX268753                  9 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 1 from Patent WO0174342.
ACCESSION   AX268753
VERSION     AX268753.1  GI:16541825
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gilchrest,B.A., Yaar,M. and Eller,M.
  TITLE     Use of locally applied dna fragments
  JOURNAL   Patent: WO 0174342-A 1 11-OCT-2001;
            TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
                     /note="Synthetic DNA Fragment"
BASE COUNT        3 a      0 c      4 g      2 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 3.2e+09;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          7 CATAC 3


RESULT 9
S50583/c
LOCUS       S50583                    9 bp    mRNA    linear   PRI 07-MAY-1993
DEFINITION  type I procollagen [human, mRNA Mutant, 9 nt].
ACCESSION   S50583
VERSION     S50583.1  GI:233928
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Tsuneyoshi,T., Westerhausen,A., Constantinou,C.D. and Prockop,D.J.
  TITLE     Substitutions for glycine alpha 1-637 and glycine alpha 2-694 of
            type I procollagen in lethal osteogenesis imperfecta. The
            conformational strain on the triple helix introduced by a glycine
            substitution can be transmitted along the helix
  JOURNAL   J. Biol. Chem. 266 (24), 15608-15613 (1991)
  MEDLINE   91340689
   PUBMED   1874719
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 50583] from the original journal article.
            This sequence comes from Fig 5A.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
     gene            1. .9
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BASE COUNT        1 a      3 c      2 g      3 t
ORIGIN

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  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          9 CATAC 5


RESULT 10
S50585/c
LOCUS       S50585                    9 bp    DNA     linear   PRI 07-MAY-1993
DEFINITION  type I procollagen [human, Genomic Mutant, 9 nt].
ACCESSION   S50585
VERSION     S50585.1  GI:233929
KEYWORDS    .
SOURCE      Homo sapiens.
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Tsuneyoshi,T., Westerhausen,A., Constantinou,C.D. and Prockop,D.J.
  TITLE     Substitutions for glycine alpha 1-637 and glycine alpha 2-694 of
            type I procollagen in lethal osteogenesis imperfecta. The
            conformational strain on the triple helix introduced by a glycine
            substitution can be transmitted along the helix
  JOURNAL   J. Biol. Chem. 266 (24), 15608-15613 (1991)
  MEDLINE   91340689
   PUBMED   1874719
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 50585] from the original journal article.
            This sequence comes from Fig 5B.
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Qy          1 CATAC 5
              |||||
Db          9 CATAC 5


RESULT 11
A18263/c
LOCUS       A18263                    10 bp    DNA     linear   PAT 12-APR-1994
DEFINITION  oligonucleotide.
ACCESSION   A18263
VERSION     A18263.1  GI:512254
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Della Valle,F., Callegaro,L. and Negro,A.
  TITLE     Process for the preparation of genetic vectors for the nerve growth
            factor expression in eukaryotic cells
  JOURNAL   Patent: EP 0432510-A 12 19-JUN-1991;
            FIDIA S.p.A
FEATURES             Location/Qualifiers
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BASE COUNT        3 a      1 c      3 g      3 t
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Qy          1 CATAC 5
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Db         10 CATAC 6


RESULT 12
AR065157
LOCUS       AR065157                  10 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5849489.
ACCESSION   AR065157
VERSION     AR065157.1  GI:5995373
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Heller,M.J.
  TITLE     Hybridization of polynucleotides conjugated with chromophores and
            fluorophores to generate donor-to-donor energy transfer system
  JOURNAL   Patent: US 5849489-A 1 15-DEC-1998;
FEATURES             Location/Qualifiers
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Qy          1 CATAC 5
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Db          4 CATAC 8


RESULT 13
AR079101/c
LOCUS       AR079101                  10 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 23 from patent US 5965409.
ACCESSION   AR079101
VERSION     AR079101.1  GI:10005847
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Pardee,A.B. and Liang,P.
  TITLE     System for comparing levels or amounts of mRNAs
  JOURNAL   Patent: US 5965409-A 23 12-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
BASE COUNT        1 a      1 c      3 g      4 t      1 others
ORIGIN

  Query Match           100.0%;  Score 5;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 6.8e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          5 CATAC 1


RESULT 14
AR079103/c
LOCUS       AR079103                  10 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 25 from patent US 5965409.
ACCESSION   AR079103
VERSION     AR079103.1  GI:10005849
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Pardee,A.B. and Liang,P.
  TITLE     System for comparing levels or amounts of mRNAs
  JOURNAL   Patent: US 5965409-A 25 12-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
BASE COUNT        1 a      2 c      3 g      3 t      1 others
ORIGIN

  Query Match           100.0%;  Score 5;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 6.8e+06;
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  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          5 CATAC 1


RESULT 15
AR098909/c
LOCUS       AR098909                  10 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 45 from patent US 6077685.
ACCESSION   AR098909
VERSION     AR098909.1  GI:12808675
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.
  TITLE     Tumor suppressor merlin and antibodies thereof
  JOURNAL   Patent: US 6077685-A 45 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
BASE COUNT        2 a      2 c      3 g      3 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 6.8e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          5 CATAC 1


Search completed: July  6, 2003, 08:29:48
Job time : 239.5 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 06:40:37 ; Search time 110.714 Seconds
(without alignments)
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Title: US-09-540-843-6
Perfect score: 5
Sequence: 1 catac 5

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2063506

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	5	100.0	5	20	AAZ10695	Oligonucleotide se
	2	5	100.0	5	20	AAZ10696	Oligonucleotide se
c	3	5	100.0	5	23	AAS14908	Melanogenesis asso
	4	5	100.0	5	23	AAS14910	Melanogenesis asso
c	5	5	100.0	7	20	AAZ10694	Oligonucleotide se
c	6	5	100.0	7	23	AAS14907	Melanogenesis asso
c	7	5	100.0	7	23	AAS14911	Melanogenesis asso
	8	5	100.0	8	22	AAD02250	Direct repeat sequ
c	9	5	100.0	9	19	AAV22350	A promoter regulat
c	10	5	100.0	9	19	AAV22283	GAS complement gen
c	11	5	100.0	9	19	AAV15899	Cyclin D transcrip
c	12	5	100.0	9	20	AAZ10692	Oligonucleotide se
c	13	5	100.0	9	23	AAS14905	Melanogenesis asso
	14	5	100.0	9	24	ABQ71504	Zinc finger protei
c	15	5	100.0	9	24	ABQ71922	Zinc finger protei
c	16	5	100.0	9	24	ABQ71958	Zinc finger protei
	17	5	100.0	10	14	AAQ43164	Donor oligomer wit
c	18	5	100.0	10	15	AAQ71104	Merlin exon 14 spl
c	19	5	100.0	10	16	AAQ97224	Oligonucleotide Ec
	20	5	100.0	10	16	AAX32625	Anticancer duplex
c	21	5	100.0	10	17	AAT35734	Primer E19 for V.d
	22	5	100.0	10	18	AAT66073	(dC-dA)n.(dG-dT)n
c	23	5	100.0	10	19	AAV50271	Yeast tag for addi
c	24	5	100.0	10	19	AAV50250	Yeast tag for addi
	25	5	100.0	10	19	AAV50184	Yeast tag for addi
	26	5	100.0	10	19	AAV50127	Yeast tag for NORF
c	27	5	100.0	10	19	AAV35934	Primer used in RAP
c	28	5	100.0	10	19	AAV35910	Primer used in RAP
c	29	5	100.0	10	20	AAX18629	p53 serial analysi
	30	5	100.0	10	20	AAV73806	Chromophore contai
	31	5	100.0	10	21	AAC73931	Human dendritic ce
	32	5	100.0	10	21	AAC74120	Human monocyte and
c	33	5	100.0	10	21	AAC74154	Human monocyte and
	34	5	100.0	10	21	AAA93858	Oligonucleotide us
c	35	5	100.0	10	21	AAA93865	Oligonucleotide us
c	36	5	100.0	10	21	AAA53110	Mouse DNA adapter
	37	5	100.0	10	21	AAA15244	Primer MR15 for mo
c	38	5	100.0	10	21	AAA56166	Human monocyte gen
c	39	5	100.0	10	21	AAA56218	Human macrophage g
	40	5	100.0	10	21	AAA56224	Human macrophage g
c	41	5	100.0	10	21	AAA56294	Human macrophage g
	42	5	100.0	10	21	AAA56321	Human macrophage g
c	43	5	100.0	10	21	AAA56331	Human macrophage g
c	44	5	100.0	10	21	AAA56407	Human macrophage g
	45	5	100.0	10	21	AAA56440	Human macrophage g

ALIGNMENTS

RESULT 1
AAZ10695/c
ID AAZ10695 standard; DNA; 5 BP.
XX
AC AAZ10695;
XX
DT 23-NOV-1999 (first entry)
XX
DE Oligonucleotide sequence that increases p53 activity in a cell.
XX
KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
KW skin cancer; ss.
XX
OS Synthetic.
XX
PN GB2336157-A.
XX
PD 13-OCT-1999.
XX
PF 24-MAR-1999; 99GB-0006758.
XX
PR 26-MAR-1998; 98US-0048927.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrest BA, Yaar M, Eller M;
XX
DR WPI; 1999-543520/46.
XX
PT DNA fragments useful for increasing p53 activity in a cell and reducing

PT susceptibility to UV-induced hyperproliferative diseases -
XX
PS Claim 11; Page 30; 44pp; English.
XX
CC AAZ10692-97 represent DNA fragments that are used for increasing p53
CC activity in a cell. The oligonucleotides are are UV mimetics and
CC protect cells against subsequent exposure to UV-irradiation or
CC chemicals. The oligonucleotides are useful for increasing p53 activity
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
CC and reducing susceptibility to skin cancer.
XX
SQ Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 5; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.3e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
|||||
Db 5 CATAC 1

RESULT 2
AAZ10696
ID AAZ10696 standard; DNA; 5 BP.
XX
AC AAZ10696;
XX
DT 23-NOV-1999 (first entry)
XX
DE Oligonucleotide sequence that increases p53 activity in a cell.
XX
KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
KW skin cancer; ss.
XX
OS Synthetic.
XX
PN GB2336157-A.
XX
PD 13-OCT-1999.
XX
PF 24-MAR-1999; 99GB-0006758.
XX
PR 26-MAR-1998; 98US-0048927.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrest BA, Yaar M, Eller M;
XX
DR WPI; 1999-543520/46.
XX
PT DNA fragments useful for increasing p53 activity in a cell and reducing
PT susceptibility to UV-induced hyperproliferative diseases -
XX
PS Claim 11; Page 30; 44pp; English.
XX
CC AAZ10692-97 represent DNA fragments that are used for increasing p53
CC activity in a cell. The oligonucleotides are are UV mimetics and
CC protect cells against subsequent exposure to UV-irradiation or
CC chemicals. The oligonucleotides are useful for increasing p53 activity
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
CC and reducing susceptibility to skin cancer.
XX
SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 5; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.3e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
|||||
Db 1 CATAC 5

RESULT 3
AAS14908/c
ID AAS14908 standard; DNA; 5 BP.
XX
AC AAS14908;
XX
DT 14-FEB-2002 (first entry)
XX
DE Melanogenesis associated oligonucleotide #4.
XX
KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS Synthetic.
XX
PN WO200174342-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10162.
XX
PR 31-MAR-2000; 2000US-0540843.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrest BA, Yaar M, Eller M;
XX
DR WPI; 2001-626338/72.
XX
PT Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT carcinoma, using specific oligonucleotides that mimic the effects of
PT ultra-violet light -
XX
PS Claim 1; Page 36; 74pp; English.
XX
CC The invention describes inhibition of mammalian epithelial cell
CC proliferation by treating cells with at least one oligonucleotide, or
CC its fragment. The compounds, which have cytostatic, anti-allergic,
CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC DNA repair processes (or a protective response to later exposure to
CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC or a tumour necrosis factor inhibitor. Probably they mimic products of
CC DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC pathway, resulting in transient arrest of cell growth, allowing more time
CC for DNA repair to occur before cell division takes place. The method is
CC especially used to treat carcinoma but may also be used to: treat other
CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC allergically mediated inflammation (atopic or contact dermatitis,
CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC cells caused by radiation or chemicals; increase melanin production
CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC promote apoptosis in epithelial cells that contain damaged DNA. Also
CC oligonucleotides that contain non-hydrolyzable backbones are used to
CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC sequence is melanogenesis associated oligonucleotide #4, a truncated
CC version of the oligonucleotide shown in AAS14906, one of the
CC oligonucleotides used to inhibit mammalian epithelial cell
CC proliferation, described in the method of the invention.
XX
SQ Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;

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  Query Match             100.0%;  Score 5;  DB 23;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          5 CATAC 1


RESULT 4
AAS14910
ID   AAS14910 standard; DNA; 5 BP.
XX
AC   AAS14910;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Melanogenesis associated oligonucleotide #6.
XX
KW   Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW   anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW   immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW   tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW   carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW   conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS   Synthetic.
XX
PN   WO200174342-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US10162.
XX
PR   31-MAR-2000; 2000US-0540843.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Gilchrest BA,  Yaar M,  Eller M;
XX
DR   WPI; 2001-626338/72.
XX
PT   Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT   carcinoma, using specific oligonucleotides that mimic the effects of
PT   ultra-violet light  -
XX
PS   Claim 1; Page 36; 74pp; English.
XX
CC   The invention describes inhibition of mammalian epithelial cell
CC   proliferation by treating cells with at least one oligonucleotide, or
CC   its fragment. The compounds, which have cytostatic, anti-allergic,
CC   anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC   immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC   DNA repair processes (or a protective response to later exposure to
CC   radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC   or a tumour necrosis factor inhibitor. Probably they mimic products of
CC   DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC   pathway, resulting in transient arrest of cell growth, allowing more time
CC   for DNA repair to occur before cell division takes place. The method is
CC   especially used to treat carcinoma but may also be used to: treat other
CC   hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC   reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC   allergically mediated inflammation (atopic or contact dermatitis,
CC   allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC   cells caused by radiation or chemicals; increase melanin production
CC   (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC   promote apoptosis in epithelial cells that contain damaged DNA. Also
CC   oligonucleotides that contain non-hydrolyzable backbones are used to
CC   inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC   sequence is melanogenesis associated oligonucleotide #6, one of the
CC   oligonucleotides used to inhibit mammalian epithelial cell proliferation,
CC   described in the method of the invention.
XX
SQ   Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;

  Query Match             100.0%;  Score 5;  DB 23;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          1 CATAC 5


RESULT 5
AAZ10694/c
ID   AAZ10694 standard; DNA; 7 BP.
XX
AC   AAZ10694;
XX
DT   23-NOV-1999  (first entry)
XX
DE   Oligonucleotide sequence that increases p53 activity in a cell.
XX
KW   p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KW   UV-induced hyperproliferative disease; psoriasis; vitiligo;
KW   atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
KW   skin cancer; ss.
XX
OS   Synthetic.
XX
PN   GB2336157-A.
XX
PD   13-OCT-1999.
XX
PF   24-MAR-1999;   99GB-0006758.
XX
PR   26-MAR-1998;   98US-0048927.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Gilchrest BA,  Yaar M,  Eller M;
XX
DR   WPI; 1999-543520/46.
XX
PT   DNA fragments useful for increasing p53 activity in a cell and reducing
PT   susceptibility to UV-induced hyperproliferative diseases -
XX
PS   Claim 11; Page 30; 44pp; English.
XX
CC   AAZ10692-97 represent DNA fragments that are used for increasing p53
CC   activity in a cell. The oligonucleotides are are UV mimetics and
CC   protect cells against subsequent exposure to UV-irradiation or
CC   chemicals. The oligonucleotides are useful for increasing p53 activity
CC   in a cell, reducing the susceptibility to UV-induced hyperproliferative
CC   diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
CC   rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
CC   and reducing susceptibility to skin cancer.
XX
SQ   Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

  Query Match             100.0%;  Score 5;  DB 20;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          6 CATAC 2


RESULT 6
AAS14907/c
ID   AAS14907 standard; DNA; 7 BP.
XX
AC   AAS14907;
```

XX
DT 14-FEB-2002 (first entry)
XX
DE Melanogenesis associated oligonucleotide #3.
XX
KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS Synthetic.
XX
PN WO200174342-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10162.
XX
PR 31-MAR-2000; 2000US-0540843.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrest BA, Yaar M, Eller M;
XX
DR WPI; 2001-626338/72.
XX
PT Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT carcinoma, using specific oligonucleotides that mimic the effects of
PT ultra-violet light -
XX
PS Claim 1; Page 36; 74pp; English.
XX
CC The invention describes inhibition of mammalian epithelial cell
CC proliferation by treating cells with at least one oligonucleotide, or
CC its fragment. The compounds, which have cytostatic, anti-allergic,
CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC DNA repair processes (or a protective response to later exposure to
CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC or a tumour necrosis factor inhibitor. Probably they mimic products of
CC DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC pathway, resulting in transient arrest of cell growth, allowing more time
CC for DNA repair to occur before cell division takes place. The method is
CC especially used to treat carcinoma but may also be used to: treat other
CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC allergically mediated inflammation (atopic or contact dermatitis,
CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC cells caused by radiation or chemicals; increase melanin production
CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC promote apoptosis in epithelial cells that contain damaged DNA. Also
CC oligonucleotides that contain non-hydrolyzable backbones are used to
CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC sequence is melanogenesis associated oligonucleotide #3, a truncated
CC version of the oligonucleotide shown in AAS14906, one of the
CC oligonucleotides used to inhibit mammalian epithelial cell
CC proliferation, described in the method of the invention.
XX
SQ Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 5; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.1e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
|||||
Db 6 CATAC 2

RESULT 7
AAS14911/c
ID AAS14911 standard; DNA; 7 BP.
XX
AC AAS14911;
XX
DT 14-FEB-2002 (first entry)
XX
DE Melanogenesis associated oligonucleotide #7.
XX
KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= a
FT /note= "Phosphorylated"
XX
PN WO200174342-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10162.
XX
PR 31-MAR-2000; 2000US-0540843.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrest BA, Yaar M, Eller M;
XX
DR WPI; 2001-626338/72.
XX
PT Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT carcinoma, using specific oligonucleotides that mimic the effects of
PT ultra-violet light -
XX
PS Claim 1; Page 38; 74pp; English.
XX
CC The invention describes inhibition of mammalian epithelial cell
CC proliferation by treating cells with at least one oligonucleotide, or
CC its fragment. The compounds, which have cytostatic, anti-allergic,
CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC DNA repair processes (or a protective response to later exposure to
CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC or a tumour necrosis factor inhibitor. Probably they mimic products of
CC DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC pathway, resulting in transient arrest of cell growth, allowing more time
CC for DNA repair to occur before cell division takes place. The method is
CC especially used to treat carcinoma but may also be used to: treat other
CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC allergically mediated inflammation (atopic or contact dermatitis,
CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC cells caused by radiation or chemicals; increase melanin production
CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC promote apoptosis in epithelial cells that contain damaged DNA. Also
CC oligonucleotides that contain non-hydrolyzable backbones are used to
CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC sequence is melanogenesis associated oligonucleotide #7, one of the
CC oligonucleotides used to inhibit mammalian epithelial cell
CC proliferation, described in the method of the invention.
XX
SQ Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 5; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.1e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CATAC 5
              |||||
Db          6 CATAC 2


RESULT 8
AAD02250
ID   AAD02250 standard; DNA; 8 BP.
XX
AC   AAD02250;
XX
DT   28-MAR-2001  (first entry)
XX
DE   Direct repeat sequence that binds to SB protein.
XX
KW   Sleeping Beauty; SB; AdSB10; adenovirus; transposase;
KW   non-integrating viral vector; cytostatic; anti-diabetic; cardiant;
KW   neuroprotective; genetic disease; gene therapy; therapy; cancer;
KW   cystic fibrosis; diabetes; cardiovascular disease; brain malfunction;
KW   genome analysis; chemotherapy; transgenic host cell; direct repeat; ds.
XX
OS   Unidentified.
XX
PN   WO200068399-A2.
XX
PD   16-NOV-2000.
XX
PF   11-MAY-2000; 2000WO-US12827.
XX
PR   11-MAY-1999;   99US-0133569.
XX
PA   (MINU ) UNIV MINNESOTA.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (MCIV/) MCIVOR R S.
PA   (HACK/) HACKETT P B.
PA   (AGUI/) AGUILAR-CORDOVA E.
XX
PI   Mcivor RS,  Hackett PB,  Aguilar-Cordova E;
XX
DR   WPI; 2001-024870/03.
XX
PT   Non-integrating (adenovirus-based) viral vectors useful in gene
PT   therapy, especially for treating patients suffering from a genetic
PT   disease, e.g. cystic fibrosis, diabetes, cardiovascular disease, cancer
PT   or brain malfunction -
XX
PS   Disclosure; Page 14; 62pp; English.
XX
CC   The patent discloses non-integrating viral vectors comprising a
CC   polynucleotide flanked by inverted repeats that bind a transposase, a
CC   transposase-encoding polynucleotide operably linked to a regulatory
CC   sequence comprising an operator, that alters expression of the
CC   transposase-encoding polynucleotide. Transposon sequences can integrate
CC   into genomic DNA whether or not the cell is dividing. AdSB10 is a SB
CC   (Sleeping Beauty) transposase-transducing adenoviral non-integrating
CC   vector. The non-integrating viral vectors are useful for treating
CC   genetic disease characterised by subnormal production of a polypeptide or
CC   RNA, e.g. for replacement of a defective gene, delivery of a polypeptide
CC   drug or supplementation of a metabolic activity. These genetic diseases
CC   include cystic fibrosis, diabetes, cardiovascular disease, cancer or
CC   brain malfunction. The non-integrating viral vectors are useful as
CC   nucleic acid delivery systems, e.g. for genome analysis or gene therapy
CC   and can also be used for applications that involve long-term production
CC   of a polypeptide. The non-integrating viral vectors are also useful for
CC   creating transgenic host cells that provide normal cells with protection
CC   against toxic side effects of chemotherapy.
CC   The sequence of the present invention is a direct repeat sequence that
CC   binds to SB protein.
XX
SQ   Sequence 8 BP; 4 A; 3 C; 0 G; 1 T; 0 other;

  Query Match             100.0%;  Score 5;  DB 22;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          2 CATAC 6


RESULT 9
AAV22350/c
ID   AAV22350 standard; RNA; 9 BP.
XX
AC   AAV22350;
XX
DT   29-JUN-1998  (first entry)
XX
DE   A promoter regulatory motif found in the utrons of the invention.
XX
KW   3' untranslated region; UTR; inhibition; gene expression; ICAM-7;
KW   interferon-gamma; IFN-gamma; major histocompatibility complex; MHC;
KW   antigen expression; gene promoter; utron; B7-1; B7-2; Fc gamma R;
KW   HIV gene expression; transplant rejection; treatment;
KW   autoimmune disease; inflammatory disease; ss.
XX
OS   Unidentified.
XX
PN   WO9744450-A1.
XX
PD   27-NOV-1997.
XX
PF   21-MAY-1997;   97WO-US09459.
XX
PR   21-MAY-1996;   96US-0646789.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Peyman JA;
XX
DR   WPI; 1998-018505/02.
XX
PT   Utrons, RNA molecules containing promoter regulatory motifs  -
PT   useful to suppress express expression from promoter of interest,
PT   specifically TSU nucleic acid suppression of MHC Class I and II gene
PT   expression
XX
PS   Claim 20; Page 20; 200pp; English.
XX
CC   The present sequence represents a promoter regulatory element,
CC   found in the utrons of the invention. Utrons are from, or are
CC   homologous to, the 3' untranslated region (UTR), of an mRNA that
CC   stimulates or inhibits a cellular response by sequence specific
CC   interactions. The utron is able to suppress constitutive and
CC   interferon-gamma (IFN-gamma) induced major histocompatibility complex
CC   (MHC) class I and class II antigen expression and expression of other
CC   antigens, the gene promoters of which contain related sequence motifs
CC   that are stimulated by the same factors which stimulate MHC class I and
CC   class II antigen expression. Such utrons can be used to regulate
CC   gene expression in a subject, e.g. a human or a cell in vitro,
CC   specifically inhibiting MHC Class I or II, ICAM-7, B7-1, B7-2,
CC   Fc gamma R, IL-2 or HIV gene expression. They can be used to inhibit
CC   transplant rejection, or treat an autoimmune or inflammatory disease or
CC   disorder.
XX
SQ   Sequence 9 BP; 3 A; 0 C; 3 G; 3 U; 0 other;

  Query Match             100.0%;  Score 5;  DB 19;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          5 CATAC 1
```

```
RESULT 10
AAV22283/c
ID   AAV22283 standard; DNA; 9 BP.
XX
AC   AAV22283;
XX
DT   29-JUN-1998  (first entry)
XX
DE   GAS complement gene promoter motif found in a trophoblast STAT utron.
XX
KW   Trophoblast STAT utron; TSU; 3' untranslated region; UTR; inhibition;
KW   interferon-gamma; IFN-gamma; major histocompatibility complex; MHC;
KW   antigen expression; gene promoter; class I; class II; IFN signalling;
KW   GAS; ISRE; interleukin-4 response element; gene expression; ICAM-7;
KW   B7-1; B7-2; Fc gamma R; HIV gene expression; transplant rejection;
KW   treatment; autoimmune disease; inflammatory disease; ss.
XX
OS   Unidentified.
XX
PN   WO9744450-A1.
XX
PD   27-NOV-1997.
XX
PF   21-MAY-1997;   97WO-US09459.
XX
PR   21-MAY-1996;   96US-0646789.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Peyman JA;
XX
DR   WPI; 1998-018505/02.
XX
PT   Utrons, RNA molecules containing promoter regulatory motifs  -
PT   useful to suppress express expression from promoter of interest,
PT   specifically TSU nucleic acid suppression of MHC Class I and II gene
PT   expression
XX
PS   Claim 22; Page 90; 200pp; English.
XX
CC   The present sequence represents a GAS complement gene promoter motif
CC   found in a trophoblast STAT utron (TSU). TSUs be isolated from a CDNA
CC   library prepared from mRNA isolated from trophoblast cells. Utrons are
CC   from, or are homologous to, the 3' untranslated region (UTR), of an mRNA
CC   that stimulates or inhibits a cellular response by sequence specific
CC   interactions. The TSU is able to suppress constitutive and
CC   interferon-gamma (IFN-gamma) induced major histocompatibility complex
CC   (MHC) class I and class II antigen expression and expression of other
CC   antigens, the gene promoters of which contain related sequence motifs
CC   that are stimulated by the same factors which stimulate MHC class I and
CC   class II antigen expression. The TSU sequence contains motifs related to
CC   IFN signalling (GAS, ISRE and interleukin-4 response elements). The
CC   nucleic acid can be used to regulate gene expression in a subject, e.g. a
CC   human or a cell in vitro, specifically inhibiting MHC Class I or II,
CC   ICAM-7, B7-1, B7-2, Fc gamma R, IL-2 or HIV gene expression. It can be
CC   used to inhibit transplant rejection, or treat an autoimmune or
CC   inflammatory disease or disorder. It can also be used to inhibit the
CC   action of STAT1-6, or a cytokine.
XX
SQ   Sequence 9 BP; 3 A; 0 C; 3 G; 3 T; 0 other;

  Query Match           100.0%;  Score 5;  DB 19;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          5 CATAC 1


RESULT 11
AAV15899/c
ID   AAV15899 standard; DNA; 9 BP.
XX
AC   AAV15899;
XX
DT   26-MAY-1998  (first entry)
XX
DE   Cyclin D transcription factor DMP1 nonamer consensus sequence.
XX
KW   cyclin D transcription factor; binding affinity; D-type cyclin; probe;
KW   cell cycle inhibitor; tumour; detection; cancer; DMP1; competitor;
KW   nonamer consensus sequence; ss.
XX
OS   Mus musculus.
OS   Homo sapiens.
XX
PN   WO9743415-A1.
XX
PD   20-NOV-1997.
XX
PF   16-MAY-1997;   97WO-US08480.
XX
PR   15-MAY-1997;   97US-0017815.
PR   16-MAY-1996;   96US-0017815.
PR   16-MAY-1996;   96US-0648837.
XX
PA   (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
PI   Hirai H,  Inoue K,  Sherr CJ;
XX
DR   WPI; 1998-008884/01.
XX
PT   Cyclin D transcription factor and related DNA - can be used to
PT   develop products for treatment of, e.g. cancer
XX
PS   Claim 3; Page 99; 120pp; English.
XX
CC   This is a nonamer consensus sequence of a cyclin D transcription factor
CC   DMP1. DMP1 is an amino acid polymer which has binding affinity for a
CC   D-type cyclin, in vitro, and for a specific DNA nucleotide sequence and
CC   is a transcription factor involved in the activation of genes that
CC   prevent cell proliferation. The DMP1 nucleic acid is operatively linked
CC   to an expression control sequence in an expression vector: The expression
CC   vector has a transcription control sequence comprising this nonamer
CC   sequence operably associated with a recombinant gene or a cassette
CC   insertion site for a recombinant gene. The vector is homologously
CC   recombined in a chromosome of a transgenic animal. A probe or a
CC   competitor in DMP1 transactivation assays is designed based on this
CC   nonamer sequence.The presence of activity of DMP1 can be determined by
CC   detecting binding of DMP1 and a probe by contacting a biological sample
CC   from a mammal with the probe under conditions that allow binding of the
CC   probe to DMP1, where the probe  contains the core sequence GTA, and where
CC   the presence or activity of DMP1 is suspected in the sample. DMP1 can
CC   function as a cell cycle inhibitor when expressed in a tumour cell.
CC   Modulating the expression of DMP1 can be used to treat tumours and other
CC   cancers. DMP1 can also be used for controlling expression of heterologous
CC   proteins. Antisense sequences and ribozymes can be used to inhibit
CC   expression of the transcription factor. Detecting the level and activity
CC   of DMP1 in cells is useful for detection of cancer cells or
CC   dysproliferative cells.
XX
SQ   Sequence 9 BP; 1 A; 3 C; 2 G; 3 T; 0 other;

  Query Match           100.0%;  Score 5;  DB 19;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          8 CATAC 4


RESULT 12
AAZ10692/c
```

```
ID   AAZ10692 standard; DNA; 9 BP.
XX
AC   AAZ10692;
XX
DT   23-NOV-1999  (first entry)
XX
DE   Oligonucleotide sequence that increases p53 activity in a cell.
XX
KW   p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KW   UV-induced hyperproliferative disease; psoriasis; vitiligo;
KW   atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
KW   skin cancer; ss.
XX
OS   Synthetic.
XX
PN   GB2336157-A.
XX
PD   13-OCT-1999.
XX
PF   24-MAR-1999;   99GB-0006758.
XX
PR   26-MAR-1998;   98US-0048927.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Gilchrest BA,  Yaar M,  Eller M;
XX
DR   WPI; 1999-543520/46.
XX
PT   DNA fragments useful for increasing p53 activity in a cell and reducing
PT   susceptibility to UV-induced hyperproliferative diseases -
XX
PS   Claim 11; Page 29; 44pp; English.
XX
CC   AAZ10692-97 represent DNA fragments that are used for increasing p53
CC   activity in a cell. The oligonucleotides are are UV mimetics and
CC   protect cells against subsequent exposure to UV-irradiation or
CC   chemicals. The oligonucleotides are useful for increasing p53 activity
CC   in a cell, reducing the susceptibility to UV-induced hyperproliferative
CC   diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
CC   rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
CC   and reducing susceptibility to skin cancer.
XX
SQ   Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;

  Query Match             100.0%;  Score 5;  DB 20;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          7 CATAC 3


RESULT 13
AAS14905/c
ID   AAS14905 standard; DNA; 9 BP.
XX
AC   AAS14905;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Melanogenesis associated oligonucleotide #1.
XX
KW   Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW   anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW   immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW   tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW   carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW   conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= g
FT                   /note= "Optionally phosphorylated"
XX
PN   WO200174342-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US10162.
XX
PR   31-MAR-2000; 2000US-0540843.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Gilchrest BA,  Yaar M,  Eller M;
XX
DR   WPI; 2001-626338/72.
XX
PT   Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT   carcinoma, using specific oligonucleotides that mimic the effects of
PT   ultra-violet light  -
XX
PS   Claim 1; Page 36; 74pp; English.
XX
CC   The invention describes inhibition of mammalian epithelial cell
CC   proliferation by treating cells with at least one oligonucleotide, or
CC   its fragment. The compounds, which have cytostatic, anti-allergic,
CC   anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC   immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC   DNA repair processes (or a protective response to later exposure to
CC   radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC   or a tumour necrosis factor inhibitor. Probably they mimic products of
CC   DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC   pathway, resulting in transient arrest of cell growth, allowing more time
CC   for DNA repair to occur before cell division takes place. The method is
CC   especially used to treat carcinoma but may also be used to: treat other
CC   hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC   reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC   allergically mediated inflammation (atopic or contact dermatitis,
CC   allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC   cells caused by radiation or chemicals; increase melanin production
CC   (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC   promote apoptosis in epithelial cells that contain damaged DNA. Also
CC   oligonucleotides that contain non-hydrolyzable backbones are used to
CC   inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC   sequence is melanogenesis associated oligonucleotide #1, one of the
CC   oligonucleotides used to inhibit mammalian epithelial cell
CC   proliferation, described in the method of the invention.
XX
SQ   Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;

  Query Match             100.0%;  Score 5;  DB 23;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATAC 5
              |||||
Db          7 CATAC 3


RESULT 14
ABQ71504
ID   ABQ71504 standard; DNA; 9 BP.
XX
AC   ABQ71504;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Zinc finger protein related oligonucleotide target SEQ ID NO:623.
XX
KW   Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
```

XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US43438.
XX
PR 20-NOV-2000; 2000US-0716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering,
PT comprises first, second and third zinc fingers, ordered from N- to
PT C-terminus -
XX
PS Example 1; Page 45; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to
CC a target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC it binds to the S1 target subsite, selecting the F2 zinc finger such
CC that it binds to the S2 target subsite, and selecting the F3 zinc
CC finger such that it binds to the S3 target subsite, thus designing (I)
CC that binds to a target site. (I) is useful for recognition of triplet
CC target subsites having the nucleotide G in the 5'-most position of the
CC subsite. (I) is useful in studying gene function, and for human
CC therapeutics and plant engineering. (I), (II) or (III) is useful in
CC therapeutic methods to modulate the expression of a target region within
CC a subject, in diagnostic methods for sequence specific detection of
CC target nucleic acid in a sample, and in assays to determined the
CC phenotype and function of gene expression. (I) has improved affinity
CC and specificity for their target sequences, as well as enhanced
CC biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC represent DNA target sequences and zinc finger peptides which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 9 BP; 2 A; 2 C; 3 G; 2 T; 0 other;

Query Match 100.0%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
|||||
Db 2 CATAC 6

RESULT 15
ABQ71922/c
ID ABQ71922 standard; DNA; 9 BP.
XX
AC ABQ71922;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2220.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.

XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US43438.
XX
PR 20-NOV-2000; 2000US-0716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering,
PT comprises first, second and third zinc fingers, ordered from N- to
PT C-terminus -
XX
PS Example 1; Page 58; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to
CC a target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC it binds to the S1 target subsite, selecting the F2 zinc finger such
CC that it binds to the S2 target subsite, and selecting the F3 zinc
CC finger such that it binds to the S3 target subsite, thus designing (I)
CC that binds to a target site. (I) is useful for recognition of triplet
CC target subsites having the nucleotide G in the 5'-most position of the
CC subsite. (I) is useful in studying gene function, and for human
CC therapeutics and plant engineering. (I), (II) or (III) is useful in
CC therapeutic methods to modulate the expression of a target region within
CC a subject, in diagnostic methods for sequence specific detection of
CC target nucleic acid in a sample, and in assays to determined the
CC phenotype and function of gene expression. (I) has improved affinity
CC and specificity for their target sequences, as well as enhanced
CC biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC represent DNA target sequences and zinc finger peptides which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 9 BP; 2 A; 0 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
|||||
Db 8 CATAC 4

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GenCore version 5.1.6

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Total number of hits satisfying chosen parameters: 2063506

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Maximum DB seq length: 40

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17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		6	100.0	6	16	AAT05734	Telomerase oligonu
2		6	100.0	6	20	AAX80998	Telomeric repeat s
3		6	100.0	6	23	AAS14915	Melanogenesis asso
c 4		6	100.0	6	23	AAS14916	Melanogenesis asso
5		6	100.0	6	24	ABN73654	Bovine embryonic g
c 6		6	100.0	7	10	AAN91439	Telomere of Arabid
c 7		6	100.0	7	10	AAN91442	Variant of Arabido
8		6	100.0	8	16	AAQ97993	Peptide nucleic ac
9		6	100.0	8	18	AAT89239	Peptide nucleic ac
10		6	100.0	8	21	AAA37558	PNA sequence #15 u
c 11		6	100.0	8	21	AAA37572	PNA sequence #30 u
12		6	100.0	8	23	AAS15436	PNA 28 inhibiting
13		6	100.0	8	23	AAS15474	PNA 34 inhibiting
14		6	100.0	9	16	AAT05735	Telomerase oligonu
15		6	100.0	9	18	AAT89240	Peptide nucleic ac
16		6	100.0	9	18	AAT93240	Telomerase substra
17		6	100.0	9	20	AAX21987	Telomere motif mim
18		6	100.0	9	21	AAA37559	PNA sequence #16 u
19		6	100.0	9	21	AAZ56813	Primer for human t
20		6	100.0	9	22	AAL20082	Human breast cance
21		6	100.0	9	23	AAS15437	PNA 29 inhibiting
c 22		6	100.0	9	24	ABK87319	Drosophila Bicoid
23		6	100.0	10	18	AAV07770	N3 to P5 oligonucl
24		6	100.0	10	18	AAV07771	N3 to P5 oligonucl
25		6	100.0	10	18	AAT89241	Peptide nucleic ac
c 26		6	100.0	10	18	AAT89249	DNA oligonucleotid
27		6	100.0	10	18	AAT89231	Peptide nucleic ac
c 28		6	100.0	10	19	AAV41382	Antisense oligonuc
c 29		6	100.0	10	20	AAZ28358	Lung cancer indica
30		6	100.0	10	20	AAX22183	Random amplified p
31		6	100.0	10	20	AAX21986	Telomere motif mim
32		6	100.0	10	20	AAX21995	Telomere motif mim
33		6	100.0	10	21	AAA56520	Human macrophage g
34		6	100.0	10	21	AAA37550	PNA sequence #7 us
c 35		6	100.0	10	21	AAA37554	Template region of
36		6	100.0	10	21	AAA37560	PNA sequence #17 u
37		6	100.0	10	21	AAA37563	PNA sequence #21 u
c 38		6	100.0	10	21	AAA37571	PNA sequence #29 u
39		6	100.0	10	21	AAZ77628	Human dendritic ce
40		6	100.0	10	21	AAZ77930	Human dendritic ce
41		6	100.0	10	21	AAZ78185	Human dendritic ce
42		6	100.0	10	21	AAZ79266	Human dendritic ce
43		6	100.0	10	21	AAZ80922	Metastatic breast
c 44		6	100.0	10	21	AAZ81372	Metastatic breast
c 45		6	100.0	10	21	AAZ81511	Metastatic breast

ALIGNMENTS

RESULT 1
AAT05734
ID AAT05734 standard; DNA; 6 BP.
XX
AC AAT05734;
XX
DT 01-FEB-1996 (first entry)
XX
DE Telomerase oligonucleotide substrate #1.
XX
KW Telomerase; proliferation; telomere; hybrid; immortalised cell; anaemia;
KW transplantation; cell therapy; treatment; AIDS; leukaemia; lymphoma; ss.
XX
OS Synthetic.
XX
PN WO9513383-A1.
XX
PD 18-MAY-1995.
XX
PF 10-NOV-1994; 94WO-US13130.
XX
PR 12-NOV-1993; 93US-0153051.
PR 12-NOV-1993; 93US-0151477.
XX
PA (GERO-) GERON CORP.
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Shay J, West MD, Wright WE;
XX
DR WPI; 1995-224051/29.
XX
PT Increasing telomere length in cells - to increase proliferative

PT capacity and therefore delay cellular senescence, useful in cell
PT therapy and transplantation
XX
PS Claim 12; Page 29; 38pp; English.
XX
CC Oligonucleotides AAT05734-7 are examples of telomerase substrates used
CC to increase the proliferative capacity of normal cells that express
CC telomerase activity. The oligonucleotides allow an increase in
CC length of telomeres in normal cells and in hybrids of normal and
CC immortalised cells. The increase in telomere length extends the
CC capacity of cells to replicate, esp. those treated ex vivo and used
CC for transplantation techniques e.g. cell therapy, for the treatment
CC of AIDS, anaemia, leukaemia or lymphoma.
XX
SQ Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;

Query Match 100.0%; Score 6; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.6e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
||||||
Db 1 TTAGGG 6

RESULT 2
AAX80998
ID AAX80998 standard; DNA; 6 BP.
XX
AC AAX80998;
XX
DT 13-SEP-1999 (first entry)
XX
DE Telomeric repeat sequence.
XX
KW Telomerase reverse transcriptase; TERT; mouse; telomere length assay;
KW immunogen; enzyme; telomerase-mediated DNA replication; human; ss.
XX
OS Homo sapiens.
XX
PN WO9927113-A1.
XX
PD 03-JUN-1999.
XX
PF 25-NOV-1998; 98WO-US25211.
XX
PR 16-MAR-1998; 98US-0042460.
PR 26-NOV-1997; 97US-0979742.
XX
PA (GERO-) GERON CORP.
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
XX
PI Allsopp R, Depinho R, Greenberg R, Morin GB;
XX
DR WPI; 1999-347722/29.
XX
PT Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and
PT nucleic acids
XX
PS Disclosure; Page 62; 135pp; English.
XX
CC The invention relates to a mouse telomerase reverse transcriptase (mTERT)
CC enzyme. Compositions containing mTERT can be used in telomere length
CC assays. Isolated mTERT is useful as an immunogen for the production of
CC monoclonal or polyclonal antibodies. The method is useful for assessing
CC the degree of purification and identification of new mTERT species, such
CC as an mTERT allele, homolog or isoform, or to screen for modulators
CC (antagonists and agonists) of telomerase-mediated DNA replication.
CC Antagonists and agonists of mTERT can be used to modify the activity of
CC other telomerase enzymes such as human TERT (hTERT).
XX
SQ Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;

Query Match 100.0%; Score 6; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.6e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
||||||
Db 1 TTAGGG 6

RESULT 3
AAS14915
ID AAS14915 standard; DNA; 6 BP.
XX
AC AAS14915;
XX
DT 14-FEB-2002 (first entry)
XX
DE Melanogenesis assocaited oligonucleotide #11.
XX
KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS Synthetic.
XX
PN WO200174342-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10162.
XX
PR 31-MAR-2000; 2000US-0540843.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrest BA, Yaar M, Eller M;
XX
DR WPI; 2001-626338/72.
XX
PT Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT carcinoma, using specific oligonucleotides that mimic the effects of
PT ultra-violet light -
XX
PS Claim 1; Page 37; 74pp; English.
XX
CC The invention describes inhibition of mammalian epithelial cell
CC proliferation by treating cells with at least one oligonucleotide, or
CC its fragment. The compounds, which have cytostatic, anti-allergic,
CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC DNA repair processes (or a protective response to later exposure to
CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC or a tumour necrosis factor inhibitor. Probably they mimic products of
CC DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC pathway, resulting in transient arrest of cell growth, allowing more time
CC for DNA repair to occur before cell division takes place. The method is
CC especially used to treat carcinoma but may also be used to: treat other
CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC allergically mediated inflammation (atopic or contact dermatitis,
CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC cells caused by radiation or chemicals; increase melanin production
CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC promote apoptosis in epithelial cells that contain damaged DNA. Also
CC oligonucleotides that contain non-hydrolyzable backbones are used to
CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC sequence is melanogenesis associated oligonucleotide #11, a truncated
CC version of the sequence representing the telomere over-hang sequence
CC (AAS14909) and one of the oligonucleotides used to inhibit mammalian
CC epithelial cell proliferation, described in the method of the invention.

```
XX
SQ   Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;

  Query Match           100.0%;  Score 6;  DB 23;  Length 6;
  Best Local Similarity  100.0%;  Pred. No. 3.6e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 4
AAS14916/c
ID   AAS14916 standard; DNA; 6 BP.
XX
AC   AAS14916;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Melanogenesis associated oligonucleotide #12.
XX
KW   Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW   anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW   immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW   tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW   carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW   conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS   Synthetic.
XX
PN   WO200174342-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US10162.
XX
PR   31-MAR-2000; 2000US-0540843.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Gilchrest BA,  Yaar M,  Eller M;
XX
DR   WPI; 2001-626338/72.
XX
PT   Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT   carcinoma, using specific oligonucleotides that mimic the effects of
PT   ultra-violet light  -
XX
PS   Claim 1; Page 37; 74pp; English.
XX
CC   The invention describes inhibition of mammalian epithelial cell
CC   proliferation by treating cells with at least one oligonucleotide, or
CC   its fragment. The compounds, which have cytostatic, anti-allergic,
CC   anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC   immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC   DNA repair processes (or a protective response to later exposure to
CC   radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC   or a tumour necrosis factor inhibitor. Probably they mimic products of
CC   DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC   pathway, resulting in transient arrest of cell growth, allowing more time
CC   for DNA repair to occur before cell division takes place. The method is
CC   especially used to treat carcinoma but may also be used to: treat other
CC   hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC   reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC   allergically mediated inflammation (atopic or contact dermatitis,
CC   allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC   cells caused by radiation or chemicals; increase melanin production
CC   (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC   promote apoptosis in epithelial cells that contain damaged DNA. Also
CC   oligonucleotides that contain non-hydrolyzable backbones are used to
CC   inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC   sequence is melanogenesis associated oligonucleotide #12, the reverse
CC   complementary sequence of AAS149015, a truncated version of the sequence
CC   representing the telomere over-hang sequence (AAS14909), described in the
CC   method of the invention.
XX
SQ   Sequence 6 BP; 2 A; 3 C; 0 G; 1 T; 0 other;

  Query Match           100.0%;  Score 6;  DB 23;  Length 6;
  Best Local Similarity  100.0%;  Pred. No. 3.6e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          6 TTAGGG 1


RESULT 5
ABN73654
ID   ABN73654 standard; cDNA; 6 BP.
XX
AC   ABN73654;
XX
DT   03-JUL-2002  (first entry)
XX
DE   Bovine embryonic germ (EG) cell cDNA EST 990913a CONTIG 1.
XX
KW   Bovine; Bos taurus; EST; expressed sequence tag; totipotence;
KW   development; gene; ss.
XX
OS   Bos taurus.
XX
PN   WO200194550-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US18576.
XX
PR   07-JUN-2000; 2000US-209874P.
PR   06-JUN-2001; 2001US-0876143.
XX
PA   (INFI-) INFIGEN INC.
XX
PI   Eilertsen KJ,  Pfister-Genskow M,  Childs L;
XX
DR   WPI; 2002-351289/38.
XX
PT   An expressed sequence tag (EST), the expression of which, or its
PT   complementary sequence, in a cell identifies the cell as a
PT   developmentally competent or incompetent cell -
XX
PS   Example 16; Page 210; 584pp; English.
XX
CC   The present invention describes an expressed sequence tag (EST), where
CC   the EST is an isolated, enriched, or purified nucleic acid sequence
CC   representing all or part of a gene, the expression of which, or its
CC   complementary sequence, in a cell identifies the cell as a
CC   developmentally competent or incompetent cell. Molecules which induce
CC   developmental competence in a cell line are useful for inducing
CC   totipotence in one or more cells. Molecules which induce developmental
CC   incompetence in a cell line are useful for preventing a full term
CC   pregnancy in an animal and inhibiting totipotence. The molecules are
CC   also useful for treating a disease in an animal by inducing development
CC   of one or more cells of the animal into a specific cell type. The
CC   present sequence represents a bovine EST which is given in the
CC   exemplification of the present invention.
XX
SQ   Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;

  Query Match           100.0%;  Score 6;  DB 24;  Length 6;
  Best Local Similarity  100.0%;  Pred. No. 3.6e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
```

```
Db          1 TTAGGG 6


RESULT 6
AAN91439/c
ID   AAN91439 standard; DNA; 7 BP.
XX
AC   AAN91439;
XX
DT   22-FEB-1990  (first entry)
XX
DE   Telomere of Arabidopsis thaliana.
XX
KW   Telomere; Arabidopsis thaliana; vector; artificial chromosomes;
KW   tandem repeat.
XX
OS   Arabidopsis thaliana.
XX
PN   WO8909219-A.
XX
PD   05-OCT-1989.
XX
PF   27-FEB-1989;   89WO-US00795.
XX
PR   24-MAR-1988;   88US-0172467.
XX
PA   (GEHO-) THE GENERAL HOSPITAL CORP.
XX
PI   Richards E,  Ausubel FM;
XX
DR   WPI; 1989-309497/42.
XX
PT   New recombinant DNA contg. eukaryotic telomere esp. from higher plant
PT   - useful as vector for specific genes and maintained in nucleus as
PT   independent replicating molecule.
XX
PS   Claim 28; page 50; 65pp; English.
XX
CC   Tandem repeats (1-1000) of the telomere are used in a vector for
CC   expressing specific genes in plants. They provide 'artificial
CC   chromosomes' which are maintained in the nucleus, so are not subjected to
CC   variable expression due to integration-position effects. They allow the
CC   integration of very foreign DNA without host range limitations.
CC   The telomere opt. contains variant repeats of CTCTAAA. The telomere is
CC   pref. the pAtT4 plasmid (ATCC 67577).
XX
SQ   Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 10;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          6 TTAGGG 1


RESULT 7
AAN91442/c
ID   AAN91442 standard; DNA; 7 BP.
XX
AC   AAN91442;
XX
DT   22-FEB-1990  (first entry)
XX
DE   Variant of Arabidopsis thaliana telomere.
XX
KW   Variant telomere; Arabidopsis thaliana; vector; artificial chromosomes;
KW   tandem repeat.
XX
OS   Arabidopsis thaliana.
XX
PN   WO8909219-A.
XX
PD   05-OCT-1989.
XX
PF   27-FEB-1989;   89WO-US00795.
XX
PR   24-MAR-1988;   88US-0172467.
XX
PA   (GEHO-) THE GENERAL HOSPITAL CORP.
XX
PI   Richards E,  Ausubel FM;
XX
DR   WPI; 1989-309497/42.
XX
PT   New recombinant DNA contg. eukaryotic telomere esp. from higher plant
PT   - useful as vector for specific genes and maintained in nucleus as
PT   independent replicating molecule.
XX
PS   Claim 35; page 50; 65pp; English.
XX
CC   The DNA is a variant of the telomere of the pAtT4 plasmid (ATCC 67577).
XX
SQ   Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 10;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          6 TTAGGG 1


RESULT 8
AAQ97993
ID   AAQ97993 standard; DNA; 8 BP.
XX
AC   AAQ97993;
XX
DT   19-OCT-1995  (first entry)
XX
DE   Peptide nucleic acid oligomer targetting HIV gene.
XX
KW   Peptide nucleic acid; PNA; HIV; human immunodeficiency virus;
KW   AIDS; antiviral; antisense; triple helix; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..8
FT                   /*tag=  a
FT                   /note= "at least one (and preferably all) of
FT                          the backbone subunits are composed of N-acetyl
FT                          N-(2-aminoethyl)glycine peptide residues, the
FT                          nucleobase being attached covalently to the
FT                          acetyl group and the peptide linkage being
FT                          formed by condensation of the glycine
FT                          carboxy group of one residue with the amino
FT                          group of the 2-aminoethyl moiety in the next
FT                          residue"
XX
PN   WO9504068-A.
XX
PD   09-FEB-1995.
XX
PF   28-JUL-1994;   94WO-US08517.
XX
PR   29-JUL-1993;   93US-0099718.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ecker DJ;
XX
DR   WPI; 1995-082179/11.
```

```
XX
PT   Oligomer hybridisable to HIV sequence and contg. peptide nucleic
PT   acid sub:unit - binds in complementary manner to DNA and RNA, and
PT   useful for modulating HIV viral activity, e.g. in treating AIDS
XX
PS   Claim 2; Page 176; 186pp; English.
XX
CC   New peptide nucleic acid (PNA) oligomers are provided which (a) consist
CC   of naturally occurring nucleobases covalently bound to a polyamide
CC   backbone and (b) hybridise to the translation initiation AUG region,
CC   5' untranslated region (5' UTR), 3' untranslated region (3' UTR),
CC   splice junctions or coding sequence of a human immunodeficiency virus
CC   gene chosen from env, gag, pol, rev and tat.
CC   The PNAs can be used to target RNA and single stranded DNA (ssDNA) to
CC   produce antisense-type gene regulation moieties. They have utility
CC   as gene-targetted drugs for modulating HIV processes. Hence they
CC   can be used to treat AIDS and other viral infections. They are also
CC   useful in diagnostic applications and as research tools.
CC   PNA oligomers have high affinity for complementary single stranded DNA.
CC   They are also able to form triple helices in which a first PNA strand
CC   binds with RNA or ssDNA and a second PNA strand binds with the resulting
CC   double helix or with the first PNA strand. The PNAs possess no
CC   significant charge and are water soluble, which facilitates cellular
CC   uptake. Further, since they contain amides of non-biological amino acids,
CC   they are biostable and resistant to enzymatic degradation by proteases.
CC   The present sequence is a specifically claimed PNA sequence
CC   (represented by the sequence of nucleobases) targetting HIV genes.
XX
SQ   Sequence 8 BP; 1 A; 0 C; 3 G; 4 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 16;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 9
AAT89239
ID   AAT89239 standard; DNA; 8 BP.
XX
AC   AAT89239;
XX
DT   12-MAY-1998  (first entry)
XX
DE   Peptide nucleic acid 14, targeted to mammalian telomerase.
XX
KW   Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
KW   inhibitor; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1..8
FT                    /*tag=  a
FT                    /note= "Sugar-phosphate backbone has been replaced by
FT                           a peptide backbone"
XX
PN   WO9738013-A1.
XX
PD   16-OCT-1997.
XX
PF   09-APR-1997;   97WO-US05931.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (GERO-) GERON CORP.
XX
PI   Corey D,  Norton JC,  Piatyszek MA,  Shay JW,  Wright WE;
XX
DR   WPI; 1997-512647/47.
XX
PT   New peptide nucleic acids hybridising to mammalian telomerase RNA -
PT   used to inhibit telomerase, for treating tumours and other
PT   proliferative diseases, also for diagnosis
XX
PS   Claim 9; Page 59; 76pp; English.
XX
CC   This sequence is a novel peptide nucleic acid (PNA), which acts as
CC   an inhibitor of mammalian, preferably human, telomerase.  The PNAs
CC   hybridise specifically to an RNA component of mammalian telomerase,
CC   and include the sequence GGG for specific hybridisation to the template
CC   region of this component.  PNAs can be used as probes to detect the
CC   RNA component of mammalian telomerase and as inhibitors of telomerase
CC   activity, especially in the treatment of cancer.
XX
SQ   Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 18;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          2 TTAGGG 7


RESULT 10
AAA37558
ID   AAA37558 standard; DNA; 8 BP.
XX
AC   AAA37558;
XX
DT   15-AUG-2000  (first entry)
XX
DE   PNA sequence #15 used to inhibit telomerase activity.
XX
KW   Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
KW   inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
KW   AIDS; HIV; fungal infection; forensic identification; detect; tumour;
KW   paternity testing; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..8
FT                   /*tag=  a
FT                   /note= "Peptide nucleic acid molecule, where
FT                          N-(2-aminoethyl)glycine units are linked to
FT                          nucleotide bases via glycine amino N through a
FT                          methylenecarbonyl linker"
XX
PN   US6046307-A.
XX
PD   04-APR-2000.
XX
PF   09-APR-1997;   97US-0838545.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Wright WE,  Piatyszek MA,  Shay JW,  Norton JC,  Corey DR;
XX
DR   WPI; 2000-292432/25.
XX
PT   New peptide nucleic acid (PNA) compounds that inhibit telomerase
PT   activity in mammalian cells is useful as probes to detect the RNA
PT   component of a mammalian telomerase  -
XX
PS   Claim 6; Column 71; 45pp; English.
XX
CC   The present sequence represents a peptide nucleic acid molecule which
CC   hybridises to the mRNA component of mammalian telomerase, and inhibits
```

```
CC   telomerase activity. Telomerase is a ribonucleoprotein enzyme that
CC   synthesizes one strand of the telomeric DNA, using as a template an 11
CC   nucleotide sequence contained within the RNA component of the enzyme. The
CC   invention relates to PNA molecules having a sequence of no more than 25
CC   bases, which include the sequence GTTAGG. The uncharged nature of the PNA
CC   backbone increases the melting temperature of associating strands,
CC   increases the rate of association with targeted nucleic acids, and
CC   affords greater resistance of degradation by proteases or nucleases. The
CC   therapeutic PNAs may be used for treating disease conditions such as
CC   cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
CC   immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
CC   syndrome) and associated pathologies, fungal infections, and other
CC   diseases characterized by abnormal telomere metabolism or telomerase
CC   activity, in combination with antineoplastic and other cytotoxic or
CC   cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
CC   used for molecular diagnostics, labelled PNAs are used as hybridization
CC   probes to detect or quantitate polynucleotides having a human telomerase
CC   RNA (hTR) sequence. PNA probes are also used for forensic identification
CC   of individuals, e.g. paternity testing, based on hTR gene restriction
CC   fragment length polymorphism (RFLP) pattern. PNAs are also useful as
CC   probes to detect the RNA component of a mammalian telomerase and as
CC   inhibitors of telomerase activity. The method of the present invention
CC   allows cancerous conditions to be detected with increased confidence and
CC   possibly at an earlier stage, before cells are detected as cancerous
CC   based on pathological characteristics. The diagnostic and prognostic
CC   methods of the present invention can be used to detect an immortal or
CC   neoplastic cell or tumour tissue or cancer of any origin, provided the
CC   cell expresses telomerase activity and its RNA component.
XX
SQ   Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 21;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          2 TTAGGG 7


RESULT 11
AAA37572/c
ID   AAA37572 standard; DNA; 8 BP.
XX
AC   AAA37572;
XX
DT   15-AUG-2000  (first entry)
XX
DE   PNA sequence #30 used to inhibit telomerase activity.
XX
KW   Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
KW   inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
KW   AIDS; HIV; fungal infection; forensic identification; detect; tumour;
KW   paternity testing; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..8
FT                   /*tag=  a
FT                   /note= "Peptide nucleic acid molecule, where
FT                          N-(2-aminoethyl)glycine units are linked to
FT                          nucleotide bases via glycine amino N through a
FT                          methylenecarbonyl linker"
XX
PN   US6046307-A.
XX
PD   04-APR-2000.
XX
PF   09-APR-1997;   97US-0838545.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Wright WE,  Piatyszek MA,  Shay JW,  Norton JC,  Corey DR;
XX
DR   WPI; 2000-292432/25.
XX
PT   New peptide nucleic acid (PNA) compounds that inhibit telomerase
PT   activity in mammalian cells is useful as probes to detect the RNA
PT   component of a mammalian telomerase -
XX
PS   Example 2; Column 33; 45pp; English.
XX
CC   The present sequence represents a peptide nucleic acid molecule which
CC   hybridises to the mRNA component of mammalian telomerase, and inhibits
CC   telomerase activity. Telomerase is a ribonucleoprotein enzyme that
CC   synthesizes one strand of the telomeric DNA, using as a template an 11
CC   nucleotide sequence contained within the RNA component of the enzyme. The
CC   invention relates to PNA molecules having a sequence of no more than 25
CC   bases, which include the sequence GTTAGG. The uncharged nature of the PNA
CC   backbone increases the melting temperature of associating strands,
CC   increases the rate of association with targeted nucleic acids, and
CC   affords greater resistance of degradation by proteases or nucleases. The
CC   therapeutic PNAs may be used for treating disease conditions such as
CC   cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
CC   immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
CC   syndrome) and associated pathologies, fungal infections, and other
CC   diseases characterized by abnormal telomere metabolism or telomerase
CC   activity, in combination with antineoplastic and other cytotoxic or
CC   cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
CC   used for molecular diagnostics, labelled PNAs are used as hybridization
CC   probes to detect or quantitate polynucleotides having a human telomerase
CC   RNA (hTR) sequence. PNA probes are also used for forensic identification
CC   of individuals, e.g. paternity testing, based on hTR gene restriction
CC   fragment length polymorphism (RFLP) pattern. PNAs are also useful as
CC   probes to detect the RNA component of a mammalian telomerase and as
CC   inhibitors of telomerase activity. The method of the present invention
CC   allows cancerous conditions to be detected with increased confidence and
CC   possibly at an earlier stage, before cells are detected as cancerous
CC   based on pathological characteristics. The diagnostic and prognostic
CC   methods of the present invention can be used to detect an immortal or
CC   neoplastic cell or tumour tissue or cancer of any origin, provided the
CC   cell expresses telomerase activity and its RNA component.
XX
SQ   Sequence 8 BP; 3 A; 4 C; 0 G; 1 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 21;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          7 TTAGGG 2


RESULT 12
AAS15436
ID   AAS15436 standard; DNA; 8 BP.
XX
AC   AAS15436;
XX
DT   14-FEB-2002  (first entry)
XX
DE   PNA 28 inhibiting human and mammalian telomerase activity.
XX
KW   Mammalian; peptide nucleic acid; probe; forensic; paternity testing;
KW   human telomerase RNA component; hTR gene RFLP pattern; cancer;
KW   inflammation; lymphoproliferative disease; autoimmune disease;
KW   neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS;
KW   human immunodeficiency virus; acquired immunodeficiency syndrome;
KW   telomere metabolism; mutant; cytostatic; anti-inflammatory;
KW   immunosuppressive; polyamide backbone; ss.
XX
OS   Homo sapiens.
```

```
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..8
FT                   /*tag=  a
FT                   /note= "This sequence is a peptide nucleic acid, i.e. it
FT                          contains a polyamide backbone instead of a
FT                          deoxyribose backbone"
XX
PN   US6294650-B1.
XX
PD   25-SEP-2001.
XX
PF   08-JUL-1999;   99US-0349532.
XX
PR   09-APR-1997;   97US-0838545.
PR   09-APR-1996;   96US-0630019.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Shay JW,  Wright WE,  Piatyszek MA,  Corey DR,  Norton JC;
XX
DR   WPI; 2001-638024/73.
XX
PT   New peptide nucleic acids that hybridises to the RNA component of
PT   mammalian telomerase, useful for treating or preventing cancer,
PT   inflammation, lymphoproliferative diseases, autoimmune disease, or
PT   neurodegenerative diseases -
XX
PS   Claim 7; Column 73; 46pp; English.
XX
CC   The present invention relates to peptide nucleic acids (PNAs), comprising
CC   a sequence of 6-25 nucleobases, that inhibit telomerase activity in
CC   mammalian cells by hybridising to the RNA component of mammalian
CC   telomerase. The PNAs are useful as probes to detect the RNA component
CC   of mammalian telomerase and as inhibitors of telomerase activity, or to
CC   detect and/or quantitate polynucleotide having the human telomerase
CC   RNA component (hTR) sequence, as well as in forensic identification of
CC   individuals, such as paternity testing or identification of criminal
CC   suspects or unknown descendants based on the hTR gene RFLP pattern. The
CC   PNA can be further used for treating or preventing cancer, inflammation,
CC   lymphoproliferative diseases, autoimmune disease, or neurodegenerative
CC   diseases. The PNAs in combination with other pharmaceuticals (such as
CC   antineoplastic or cytostatic agents) can be used for treating neoplasia,
CC   hyperplasia, human immunodeficiency virus (HIV) infections, acquired
CC   immunodeficiency syndrome (AIDS) and associated pathologies, and other
CC   diseases characterised by abnormal telomere metabolism or telomerase
CC   activity. The present sequence represents one of the PNA sequences
CC   of the invention.
XX
SQ   Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 23;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          2 TTAGGG 7


RESULT 13
AAS15474
ID   AAS15474 standard; DNA; 8 BP.
XX
AC   AAS15474;
XX
DT   14-FEB-2002  (first entry)
XX
DE   PNA 34 inhibiting human and mammalian telomerase activity.
XX
KW   Mammalian; peptide nucleic acid; probe; forensic; paternity testing;
KW   human telomerase RNA component; hTR gene RFLP pattern; cancer;
KW   inflammation; lymphoproliferative disease; autoimmune disease;
KW   neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS;
KW   human immunodeficiency virus; acquired immunodeficiency syndrome;
KW   telomere metabolism; mutant; cytostatic; anti-inflammatory;
KW   immunosuppressive; polyamide backbone; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..8
FT                   /*tag=  a
FT                   /note= "This sequence is a peptide nucleic acid, i.e. it
FT                          contains a polyamide backbone instead of a
FT                          deoxyribose backbone"
FT   modified_base   1
FT                   /*tag=  b
FT                   /note= "N= 1-50 peptide nucleic acid nucleobases,
FT                          selected from U, T, A, G, C or i"
FT   modified_base   8
FT                   /*tag=  c
FT                   /note= "N= 1-50 peptide nucleic acid nucleobases,
FT                          selected from U, T, A, G, C or i"
XX
PN   US6294650-B1.
XX
PD   25-SEP-2001.
XX
PF   08-JUL-1999;   99US-0349532.
XX
PR   09-APR-1997;   97US-0838545.
PR   09-APR-1996;   96US-0630019.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Shay JW,  Wright WE,  Piatyszek MA,  Corey DR,  Norton JC;
XX
DR   WPI; 2001-638024/73.
XX
PT   New peptide nucleic acids that hybridises to the RNA component of
PT   mammalian telomerase, useful for treating or preventing cancer,
PT   inflammation, lymphoproliferative diseases, autoimmune disease, or
PT   neurodegenerative diseases -
XX
PS   Disclosure; Column 59; 46pp; English.
XX
CC   The present invention relates to peptide nucleic acids (PNAs), comprising
CC   a sequence of 6-25 nucleobases, that inhibit telomerase activity in
CC   mammalian cells by hybridising to the RNA component of mammalian
CC   telomerase. The PNAs are useful as probes to detect the RNA component
CC   of mammalian telomerase and as inhibitors of telomerase activity, or to
CC   detect and/or quantitate polynucleotide having the human telomerase
CC   RNA component (hTR) sequence, as well as in forensic identification of
CC   individuals, such as paternity testing or identification of criminal
CC   suspects or unknown descendants based on the hTR gene RFLP pattern. The
CC   PNA can be further used for treating or preventing cancer, inflammation,
CC   lymphoproliferative diseases, autoimmune disease, or neurodegenerative
CC   diseases. The PNAs in combination with other pharmaceuticals (such as
CC   antineoplastic or cytostatic agents) can be used for treating neoplasia,
CC   hyperplasia, human immunodeficiency virus (HIV) infections, acquired
CC   immunodeficiency syndrome (AIDS) and associated pathologies, and other
CC   diseases characterised by abnormal telomere metabolism or telomerase
CC   activity. The present sequence represents one of the PNA sequences
CC   of the invention.
CC   Note: The present sequence is given in the SEQ ID listing but is not
CC   mentioned elsewhere in the patent.
XX
SQ   Sequence 8 BP; 1 A; 0 C; 3 G; 2 T; 2 other;

  Query Match             100.0%;  Score 6;  DB 23;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 TTAGGG 6
              ||||||
Db          2 TTAGGG 7


RESULT 14
AAT05735
ID   AAT05735 standard; DNA; 9 BP.
XX
AC   AAT05735;
XX
DT   01-FEB-1996  (first entry)
XX
DE   Telomerase oligonucleotide substrate #2.
XX
KW   Telomerase; proliferation; telomere; hybrid; immortalised cell; anaemia;
KW   transplantation; cell therapy; treatment; AIDS; leukaemia; lymphoma; ss.
XX
OS   Synthetic.
XX
PN   WO9513383-A1.
XX
PD   18-MAY-1995.
XX
PF   10-NOV-1994;   94WO-US13130.
XX
PR   12-NOV-1993;   93US-0153051.
PR   12-NOV-1993;   93US-0151477.
XX
PA   (GERO-) GERON CORP.
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Shay J,  West MD,  Wright WE;
XX
DR   WPI; 1995-224051/29.
XX
PT   Increasing telomere length in cells  - to increase proliferative
PT   capacity and therefore delay cellular senescence, useful in cell
PT   therapy and transplantation
XX
PS   Claim 12; Page 29; 38pp; English.
XX
CC   Oligonucleotides AAT05734-7 are examples of telomerase substrates used
CC   to increase the proliferative capacity of normal cells that express
CC   telomerase activity.  The oligonucleotides allow an increase in
CC   length of telomeres in normal cells and in hybrids of normal and
CC   immortalised cells.  The increase in telomere length extends the
CC   capacity of cells to replicate, esp. those treated ex vivo and used
CC   for transplantation techniques e.g. cell therapy, for the treatment
CC   of AIDS, anaemia, leukaemia or lymphoma.
XX
SQ   Sequence 9 BP; 2 A; 0 C; 3 G; 4 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 16;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 15
AAT89240
ID   AAT89240 standard; DNA; 9 BP.
XX
AC   AAT89240;
XX
DT   12-MAY-1998  (first entry)
XX
DE   Peptide nucleic acid 15, targeted to mammalian telomerase.
XX
KW   Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
KW   inhibitor; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1..9
FT                    /*tag=  a
FT                    /note= "Sugar-phosphate backbone has been replaced by
FT                           a peptide backbone"
XX
PN   WO9738013-A1.
XX
PD   16-OCT-1997.
XX
PF   09-APR-1997;   97WO-US05931.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (GERO-) GERON CORP.
XX
PI   Corey D,  Norton JC,  Piatyszek MA,  Shay JW,  Wright WE;
XX
DR   WPI; 1997-512647/47.
XX
PT   New peptide nucleic acids hybridising to mammalian telomerase RNA -
PT   used to inhibit telomerase, for treating tumours and other
PT   proliferative diseases, also for diagnosis
XX
PS   Claim 9; Page 59; 76pp; English.
XX
CC   This sequence is a novel peptide nucleic acid (PNA), which acts as
CC   an inhibitor of mammalian, preferably human, telomerase.  The PNAs
CC   hybridise specifically to an RNA component of mammalian telomerase,
CC   and include the sequence GGG for specific hybridisation to the template
CC   region of this component.  PNAs can be used as probes to detect the
CC   RNA component of mammalian telomerase and as inhibitors of telomerase
CC   activity, especially in the treatment of cancer.
XX
SQ   Sequence 9 BP; 2 A; 0 C; 4 G; 3 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 18;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          3 TTAGGG 8


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Job time : 135.107 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Title: US-09-540-843-11
Perfect score: 6
Sequence: 1 ttaggg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 774614

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: gb_sy:*
13: gb_un:*
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35: em_htg_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	6	100.0	6	6	AX055801	AX055801 Sequence
	2	6	100.0	6	6	AX058275	AX058275 Sequence
	3	6	100.0	6	6	AX175285	AX175285 Sequence
	4	6	100.0	6	6	AX268763	AX268763 Sequence
c	5	6	100.0	6	6	AX268764	AX268764 Sequence
	6	6	100.0	10	6	AR026485	AR026485 Sequence
	7	6	100.0	10	6	AX152177	AX152177 Sequence
c	8	6	100.0	10	6	AX153381	AX153381 Sequence
c	9	6	100.0	10	6	AX153382	AX153382 Sequence
c	10	6	100.0	10	6	AX153383	AX153383 Sequence
	11	6	100.0	10	6	AX153524	AX153524 Sequence
	12	6	100.0	10	6	BD011231	BD011231 Human tel
	13	6	100.0	10	6	E36980	E36980 Human telom
c	14	6	100.0	11	6	AR016034	AR016034 Sequence
	15	6	100.0	11	6	AR026486	AR026486 Sequence
c	16	6	100.0	11	6	AR026487	AR026487 Sequence
c	17	6	100.0	11	6	AR059195	AR059195 Sequence
c	18	6	100.0	11	6	AR075506	AR075506 Sequence
c	19	6	100.0	11	6	AR161904	AR161904 Sequence
c	20	6	100.0	11	6	AX033373	AX033373 Sequence
	21	6	100.0	11	6	AX268757	AX268757 Sequence
c	22	6	100.0	11	6	AX268761	AX268761 Sequence
	23	6	100.0	11	6	AX283296	AX283296 Sequence
c	24	6	100.0	11	6	AX394462	AX394462 Sequence
	25	6	100.0	11	6	AX394499	AX394499 Sequence
	26	6	100.0	11	6	AX471710	AX471710 Sequence
c	27	6	100.0	11	6	BD003369	BD003369 Mammalian
c	28	6	100.0	11	6	I31749	I31749 Sequence 2
c	29	6	100.0	12	6	A21302	A21302 Nucleotide
	30	6	100.0	12	6	AR026476	AR026476 Sequence
c	31	6	100.0	12	6	AR026477	AR026477 Sequence
c	32	6	100.0	12	6	AR026480	AR026480 Sequence
c	33	6	100.0	12	6	AR050933	AR050933 Sequence
	34	6	100.0	12	6	AR050934	AR050934 Sequence
c	35	6	100.0	12	6	AR050938	AR050938 Sequence
	36	6	100.0	12	6	AR059223	AR059223 Sequence
c	37	6	100.0	12	6	AR059544	AR059544 Sequence
	38	6	100.0	12	6	AR059545	AR059545 Sequence
	39	6	100.0	12	6	AR075547	AR075547 Sequence
c	40	6	100.0	12	6	AR134878	AR134878 Sequence
	41	6	100.0	12	6	AR134879	AR134879 Sequence
c	42	6	100.0	12	6	AR199363	AR199363 Sequence
	43	6	100.0	12	6	AR200885	AR200885 Sequence
c	44	6	100.0	12	6	AR204552	AR204552 Sequence
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ALIGNMENTS

RESULT 1
AX055801/c
LOCUS AX055801 6 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 5 from Patent WO0073420.
ACCESSION AX055801
VERSION AX055801.1 GI:12228914
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 6)
AUTHORS Hahn,W.C. and Weinberg,R.A.
TITLE Creation of human tumorigenic cells and uses therefor
JOURNAL Patent: WO 0073420-A 5 07-DEC-2000;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; DANA-FARBER

CANCER INSTITUTE, INC. (US)
FEATURES Location/Qualifiers
source 1. .6
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic primer"
BASE COUNT 2 a 3 c 0 g 1 t
ORIGIN

Query Match 100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
||||||
Db 6 TTAGGG 1

RESULT 2
AX058275
LOCUS AX058275 6 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 10 from Patent WO0074667.
ACCESSION AX058275
VERSION AX058275.1 GI:12310774
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 6)
AUTHORS Au,J.L. and Wientjes,G.
TITLE Compositions active in telomere damage comprising a taxane and telomerase inhibitor
JOURNAL Patent: WO 0074667-A 10 14-DEC-2000;
Au, Jessie L.S. (US) ; Wientjes, Guillaume (US)
FEATURES Location/Qualifiers
source 1. .6
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer/probe"
BASE COUNT 1 a 0 c 3 g 2 t
ORIGIN

Query Match 100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
||||||
Db 1 TTAGGG 6

RESULT 3
AX175285
LOCUS AX175285 6 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 49 from Patent WO0144465.
ACCESSION AX175285
VERSION AX175285.1 GI:14598653
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 6)
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 49 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES Location/Qualifiers
source 1. .6
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 1 a 0 c 3 g 2 t
ORIGIN

Query Match 100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
||||||
Db 1 TTAGGG 6

RESULT 4
AX268763
LOCUS AX268763 6 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 11 from Patent WO0174342.
ACCESSION AX268763
VERSION AX268763.1 GI:16541835
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Gilchrest,B.A., Yaar,M. and Eller,M.
TITLE Use of locally applied dna fragments
JOURNAL Patent: WO 0174342-A 11 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES Location/Qualifiers
source 1. .6
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic DNA Fragment"
BASE COUNT 1 a 0 c 3 g 2 t
ORIGIN

Query Match 100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
||||||
Db 1 TTAGGG 6

RESULT 5
AX268764/c
LOCUS AX268764 6 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 12 from Patent WO0174342.
ACCESSION AX268764
VERSION AX268764.1 GI:16541836
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Gilchrest,B.A., Yaar,M. and Eller,M.
TITLE Use of locally applied dna fragments
JOURNAL Patent: WO 0174342-A 12 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES Location/Qualifiers
source 1. .6
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic DNA Fragment"
BASE COUNT 2 a 3 c 0 g 1 t
ORIGIN

Query Match 100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
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Db 6 TTAGGG 1

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RESULT 6
AR026485
LOCUS       AR026485                 10 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 10 from patent US 5856096.
ACCESSION   AR026485
VERSION     AR026485.1  GI:5937325
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Windle,B.E., Qiu,M., Chen,S.-F., Fletcher,T.M. and Maine,I.
  TITLE     Rapid and sensitive assays for detecting and distinguishing between
            processive and non-processive telomerase activities
  JOURNAL   Patent: US 5856096-A 10 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
BASE COUNT        2 a      0 c      4 g      4 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 3.9e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 7
AX152177
LOCUS       AX152177                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 92 from Patent WO0138577.
ACCESSION   AX152177
VERSION     AX152177.1  GI:14533828
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 92 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      2 c      3 g      2 t
ORIGIN

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Qy          1 TTAGGG 6
              ||||||
Db          2 TTAGGG 7


RESULT 8
AX153381/c
LOCUS       AX153381                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1296 from Patent WO0138577.
ACCESSION   AX153381
VERSION     AX153381.1  GI:14535032
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1296 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      3 c      0 g      2 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          8 TTAGGG 3


RESULT 9
AX153382/c
LOCUS       AX153382                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1297 from Patent WO0138577.
ACCESSION   AX153382
VERSION     AX153382.1  GI:14535033
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1297 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      3 c      0 g      2 t
ORIGIN

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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          8 TTAGGG 3


RESULT 10
AX153383/c
LOCUS       AX153383                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1298 from Patent WO0138577.
ACCESSION   AX153383
VERSION     AX153383.1  GI:14535034
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1298 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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BASE COUNT        5 a      3 c      0 g      2 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          8 TTAGGG 3


RESULT 11
AX153524
LOCUS       AX153524                10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1439 from Patent WO0138577.
ACCESSION   AX153524
VERSION     AX153524.1  GI:14535175
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1439 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      1 c      5 g      3 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          5 TTAGGG 10


RESULT 12
BD011231
LOCUS       BD011231                10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Human telomerase catalytic subunit.
ACCESSION   BD011231
VERSION     BD011231.1  GI:18639604
KEYWORDS    JP 2001081042-A/188.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
            Harley,C.B. and Andrews,W.H.
  TITLE     Human telomerase catalytic subunit
  JOURNAL   Patent: JP 2001081042-A 188 27-MAR-2001;
            GERON CORP,UNIVERSITY TECHNOLOGY CORP
COMMENT     OS   Unidentified
            PN   JP 2001081042-A/188
            PD   27-MAR-2001
            PF   27-JUL-2000 JP 2000227474
            PR   01-OCT-1996 US    08/724643,18-APR-1997 US    08/844419 PR
            25-APR-1997 US    08/846017,06-MAY-1997 US    08/851843 PR
            09-MAY-1997 US    08/854050,14-AUG-1997 US    08/911312 PR
            14-AUG-1997 US    08/912951,14-AUG-1997 US    08/915503 PI   THOMAS
            R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI   GREG B
            MORIN,
            PI   CALVIN B HARLEY,WILLIAM H ANDREWS
            PC   A61K38/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00,A61P43/00,
            PC   C07K5/10,
            PC   C07K5/107,C07K5/117,C07K7/06,C07K7/08,C07K16/40,C12N9/12, PC
            C12N15/09,
            PC   C12Q1/02,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC
            G01N33/53,
            PC   G01N33/566,G01N33/573//C12P21/08,A61K37/02,C12N15/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
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            FT   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      0 c      4 g      4 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 6;  Length 10;
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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 13
E36980
LOCUS       E36980                  10 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Human telomerase catalytic subunit promoter.
ACCESSION   E36980
VERSION     E36980.1  GI:13022943
KEYWORDS    JP 1999253177-A/188.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
            Calvin,B.H. and William,H.A.
  TITLE     Human telomerase catalytic subunit promoter
  JOURNAL   Patent: JP 1999253177-A 188 21-SEP-1999;
            JERON CORP,UNIVERSITY TECHNOLOGY CORP
COMMENT     OS   Unidentified
            PN   JP 1999253177-A/188
            PD   21-SEP-1999
            PF   15-OCT-1998 JP 1998320169
            PR   01-OCT-1996 US   08/724.643,18-APR-1997 US   08/844.419, PR
            25-APR-1997 US   08/846.017,06-MAY-1997 US   08/851.843, PR
            09-MAY-1997 US   08/854.050,14-AUG-1997 US   08/911.312, PR
            14-AUG-1997 US   08/912.951,14-AUG-1997 US   08/915.503 PI   THOMAS
            R SECHI,JOCHIMU RINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI   GREG B
            MORIN,
            PI   CALVIN B HAREI,WILLIAM H ANDREWS
            PC   C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,
            PC   C12Q1/02,
            PC   C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC
              C07K16/40,
            PC   C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,(C12N1/19, PC
            C12R1:84),
            PC   (C12N1/21,C12R1:19),(C12N9/12,C12R1:19),(C12N9/12,C12R1:84),
            PC   (C12N9/12,C12R1:91),C12N15/00,A61K37/64,C12N5/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      0 c      4 g      4 t
ORIGIN
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  Best Local Similarity   100.0%;  Pred. No. 3.9e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 14
AR016034/c
LOCUS       AR016034                  11 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 2 from patent US 5776679.
ACCESSION   AR016034
VERSION     AR016034.1  GI:3972311
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
  TITLE     Assays for the DNA component of human telomerase
  JOURNAL   Patent: US 5776679-A 2 07-JUL-1998;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
BASE COUNT        4 a      5 c      0 g      2 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 3.8e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db         10 TTAGGG 5


RESULT 15
AR026486
LOCUS       AR026486                  11 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 11 from patent US 5856096.
ACCESSION   AR026486
VERSION     AR026486.1  GI:5937326
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Windle,B.E., Qiu,M., Chen,S.-F., Fletcher,T.M. and Maine,I.
  TITLE     Rapid and sensitive assays for detecting and distinguishing between
            processive and non-processive telomerase activities
  JOURNAL   Patent: US 5856096-A 11 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
BASE COUNT        2 a      0 c      5 g      4 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          2 TTAGGG 7


Search completed: July  6, 2003, 08:29:51
Job time : 286 secs
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Job time : 65.5714 secs

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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          6 TTAGGG 1


RESULT 14
US-10-044-692-294
; Sequence 294, Application US/10044692
; Publication No. US20030096344A1
;   GENERAL INFORMATION:
;        APPLICANT: Cech, Thomas R.
;                   Lingner, Joachim
;                   Nakamura, Toru
;                   Chapman, Karen B.
;                   Morin, Gregg B.
;                   Harley, Calvin
;                   Andrews, William H.
;        TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:  DIAGNOSTIC AND
;                            THERAPEUTIC METHODS
;        NUMBER OF SEQUENCES: 335
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, 8th Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/044,692
;             FILING DATE: 11-Jan-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/912,951
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: US 08/854,050
;             FILING DATE: 09-MAY-1997
;             APPLICATION NUMBER: US 08/851,843
;             FILING DATE: 06-MAY-1997
;             APPLICATION NUMBER: US 08/846,017
;             FILING DATE: 25-APR-1997
;             APPLICATION NUMBER: US 08/844,419
;             FILING DATE: 18-APR-1997
;             APPLICATION NUMBER: US 08/724,643
;             FILING DATE: 01-OCT-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Apple,  Randolph T.
;             REGISTRATION NUMBER: 36,429
;             REFERENCE/DOCKET NUMBER: 015389-002600US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 294:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 10 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 294:
US-10-044-692-294

  Query Match           100.0%;  Score 6;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 15
US-10-044-539-294
; Sequence 294, Application US/10044539
; Publication No. US20030100093A1
;   GENERAL INFORMATION:
;        APPLICANT: Cech, Thomas R.
;                   Lingner, Joachim
;                   Nakamura, Toru
;                   Chapman, Karen B.
;                   Morin, Gregg B.
;                   Harley, Calvin
;                   Andrews, William H.
;        TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:  DIAGNOSTIC AND
;                            THERAPEUTIC METHODS
;        NUMBER OF SEQUENCES: 335
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, 8th Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/044,539
;             FILING DATE: 11-Jan-2002
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/912,951
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: US 08/854,050
;             FILING DATE: 09-MAY-1997
;             APPLICATION NUMBER: US 08/851,843
;             FILING DATE: 06-MAY-1997
;             APPLICATION NUMBER: US 08/846,017
;             FILING DATE: 25-APR-1997
;             APPLICATION NUMBER: US 08/844,419
;             FILING DATE: 18-APR-1997
;             APPLICATION NUMBER: US 08/724,643
;             FILING DATE: 01-OCT-1996.
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Apple,  Randolph T.
;             REGISTRATION NUMBER: 36,429
;             REFERENCE/DOCKET NUMBER: 015389-002600US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 294:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 10 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 294:
US-10-044-539-294

  Query Match           100.0%;  Score 6;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6
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Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 10
US-09-730-893-6
; Sequence 6, Application US/09730893
; Patent No. US20020107258A1
; GENERAL INFORMATION:
;  APPLICANT: KERWIN, SEAN M.
;  APPLICANT:  FEDOROFF, OLEG Y.
;  APPLICANT:  SALAZAR, MIGUEL
;  APPLICANT:  HURLEY, LAURENCE H.
;  TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
;  TITLE OF INVENTION:  G-QUADRUPLEX-INTERACTION COMPOUND
;  FILE REFERENCE: UTSB:679USC1
;  CURRENT APPLICATION NUMBER: US/09/730,893
;  CURRENT FILING DATE:  2000-12-05
;  PRIOR APPLICATION NUMBER: 09/244,675
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: 60/073,629
;  PRIOR FILING DATE: 1998-04-02
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-09-730-893-6

  Query Match            100.0%;  Score 6;  DB 10;  Length 7;
  Best Local Similarity  100.0%;  Pred. No. 2.2e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
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Db          1 TTAGGG 6


RESULT 11
US-09-940-173A-4
; Sequence 4, Application US/09940173A
; Publication No. US20030040525A1
; GENERAL INFORMATION:
;  APPLICANT: KERWIN, SEAN M.
;  APPLICANT:  FEDOROFF, OLEG Y.
;  APPLICANT:  SALAZAR, MIGUEL
;  APPLICANT:  HURLEY, LAURENCE H.
;  TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
;  TITLE OF INVENTION:  G-QUADRUPLEX-INTERACTION COMPOUND
;  FILE REFERENCE: UTSB:679USD2
;  CURRENT APPLICATION NUMBER: US/09/940,173A
;  CURRENT FILING DATE:  2002-06-24
;  PRIOR APPLICATION NUMBER: 09/730,893
;  PRIOR FILING DATE: 2000-12-05
;  PRIOR APPLICATION NUMBER: 09/244,675
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: 60/073,629
;  PRIOR FILING DATE: 1998-04-02
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-09-940-173A-4

  Query Match            100.0%;  Score 6;  DB 9;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 1.9e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 12
US-09-730-893-4
; Sequence 4, Application US/09730893
; Patent No. US20020107258A1
; GENERAL INFORMATION:
;  APPLICANT: KERWIN, SEAN M.
;  APPLICANT:  FEDOROFF, OLEG Y.
;  APPLICANT:  SALAZAR, MIGUEL
;  APPLICANT:  HURLEY, LAURENCE H.
;  TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
;  TITLE OF INVENTION:  G-QUADRUPLEX-INTERACTION COMPOUND
;  FILE REFERENCE: UTSB:679USC1
;  CURRENT APPLICATION NUMBER: US/09/730,893
;  CURRENT FILING DATE:  2000-12-05
;  PRIOR APPLICATION NUMBER: 09/244,675
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: 60/073,629
;  PRIOR FILING DATE: 1998-04-02
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-09-730-893-4

  Query Match            100.0%;  Score 6;  DB 10;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 1.9e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 13
US-09-728-574-19/c
; Sequence 19, Application US/09728574
; Patent No. US20020137036A1
; GENERAL INFORMATION:
;  APPLICANT: Stratagene
;  TITLE OF INVENTION: Methods for Detection of a Target Nucleic Acid By Capture
;  FILE REFERENCE: 25436/1660
;  CURRENT APPLICATION NUMBER: US/09/728,574
;  CURRENT FILING DATE:  2000-11-30
;  PRIOR APPLICATION NUMBER: US 09/728574
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Drosophila sp.
;   FEATURE:
;   NAME/KEY: bicoid DNA binding site
;   LOCATION: (1)..(9)
US-09-728-574-19

  Query Match            100.0%;  Score 6;  DB 10;  Length 9;
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  Best Local Similarity   100.0%;  Pred. No. 2.5e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
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Db          1 TTAGGG 6


RESULT 6
US-09-817-387-29
; Sequence 29, Application US/09817387
; Patent No. US20010039263A1
; GENERAL INFORMATION:
;  APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin
;  TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof
;  FILE REFERENCE: 101195-24
;  CURRENT APPLICATION NUMBER: US/09/817,387
;  CURRENT FILING DATE:  2001-03-26
;  PRIOR APPLICATION NUMBER: DE 197 20 151.2
;  PRIOR FILING DATE: 1997-05-02
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  telomeric
;   OTHER INFORMATION: DNA of man
US-09-817-387-29

  Query Match             100.0%;  Score 6;  DB 10;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 7
US-09-735-363A-49
; Sequence 49, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
;  APPLICANT: Filion, Mario
;  APPLICANT:  Phillip, Nigel
;  TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
;  FILE REFERENCE: 02811-0181
;  CURRENT APPLICATION NUMBER: US/09/735,363A
;  CURRENT FILING DATE:  2000-12-12
;  PRIOR APPLICATION NUMBER: 60/170,325
;  PRIOR FILING DATE: 1999-12-13
;  PRIOR APPLICATION NUMBER: 60/228,925
;  PRIOR FILING DATE: 2000-08-29
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 49
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-49

  Query Match             100.0%;  Score 6;  DB 10;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 8
US-09-730-893-1
; Sequence 1, Application US/09730893
; Patent No. US20020107258A1
; GENERAL INFORMATION:
;  APPLICANT: KERWIN, SEAN M.
;  APPLICANT:  FEDOROFF, OLEG Y.
;  APPLICANT:  SALAZAR, MIGUEL
;  APPLICANT:  HURLEY, LAURENCE H.
;  TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
;  TITLE OF INVENTION:  G-QUADRUPLEX-INTERACTION COMPOUND
;  FILE REFERENCE: UTSB:679USC1
;  CURRENT APPLICATION NUMBER: US/09/730,893
;  CURRENT FILING DATE:  2000-12-05
;  PRIOR APPLICATION NUMBER: 09/244,675
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: 60/073,629
;  PRIOR FILING DATE: 1998-04-02
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-09-730-893-1

  Query Match             100.0%;  Score 6;  DB 10;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 9
US-09-940-173A-6
; Sequence 6, Application US/09940173A
; Publication No. US20030040525A1
; GENERAL INFORMATION:
;  APPLICANT: KERWIN, SEAN M.
;  APPLICANT:  FEDOROFF, OLEG Y.
;  APPLICANT:  SALAZAR, MIGUEL
;  APPLICANT:  HURLEY, LAURENCE H.
;  TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
;  TITLE OF INVENTION:  G-QUADRUPLEX-INTERACTION COMPOUND
;  FILE REFERENCE: UTSB:679USD2
;  CURRENT APPLICATION NUMBER: US/09/940,173A
;  CURRENT FILING DATE:  2002-06-24
;  PRIOR APPLICATION NUMBER: 09/730,893
;  PRIOR FILING DATE: 2000-12-05
;  PRIOR APPLICATION NUMBER: 09/244,675
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: 60/073,629
;  PRIOR FILING DATE: 1998-04-02
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-09-940-173A-6

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  Best Local Similarity   100.0%;  Pred. No. 2.2e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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RESULT 2
US-10-122-630-12/c
; Sequence 12, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-018
;  CURRENT APPLICATION NUMBER: US/10/122,630
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 08/467,012
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US96/08386
;  PRIOR FILING DATE: 1996-06-03
;  PRIOR APPLICATION NUMBER: US 09/048,927
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-12

  Query Match             100.0%;  Score 6;  DB 9;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
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Db          6 TTAGGG 1


RESULT 3
US-10-122-633-11
; Sequence 11, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-11

  Query Match             100.0%;  Score 6;  DB 9;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 4
US-10-122-633-12/c
; Sequence 12, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-12

  Query Match             100.0%;  Score 6;  DB 9;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          6 TTAGGG 1


RESULT 5
US-09-940-173A-1
; Sequence 1, Application US/09940173A
; Publication No. US20030040525A1
; GENERAL INFORMATION:
;  APPLICANT: KERWIN, SEAN M.
;  APPLICANT:  FEDOROFF, OLEG Y.
;  APPLICANT:  SALAZAR, MIGUEL
;  APPLICANT:  HURLEY, LAURENCE H.
;  TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
;  TITLE OF INVENTION:  G-QUADRUPLEX-INTERACTION COMPOUND
;  FILE REFERENCE: UTSB:679USD2
;  CURRENT APPLICATION NUMBER: US/09/940,173A
;  CURRENT FILING DATE:  2002-06-24
;  PRIOR APPLICATION NUMBER: 09/730,893
;  PRIOR FILING DATE: 2000-12-05
;  PRIOR APPLICATION NUMBER: 09/244,675
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: 60/073,629
;  PRIOR FILING DATE: 1998-04-02
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-09-940-173A-1

  Query Match             100.0%;  Score 6;  DB 9;  Length 6;
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 08:30:00 ; Search time 65.5714 Seconds
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Title: US-09-540-843-11
Perfect score: 6
Sequence: 1 ttaggg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 816406

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	6	100.0	6	9	US-10-122-630-11	Sequence 11, Appl
c	2	6	100.0	6	9	US-10-122-630-12	Sequence 12, Appl
	3	6	100.0	6	9	US-10-122-633-11	Sequence 11, Appl
c	4	6	100.0	6	9	US-10-122-633-12	Sequence 12, Appl
	5	6	100.0	6	9	US-09-940-173A-1	Sequence 1, Appli
	6	6	100.0	6	10	US-09-817-387-29	Sequence 29, Appl
	7	6	100.0	6	10	US-09-735-363A-49	Sequence 49, Appl
	8	6	100.0	6	10	US-09-730-893-1	Sequence 1, Appli
	9	6	100.0	7	9	US-09-940-173A-6	Sequence 6, Appli
	10	6	100.0	7	10	US-09-730-893-6	Sequence 6, Appli
	11	6	100.0	8	9	US-09-940-173A-4	Sequence 4, Appli
	12	6	100.0	8	10	US-09-730-893-4	Sequence 4, Appli
c	13	6	100.0	9	10	US-09-728-574-19	Sequence 19, Appl
	14	6	100.0	10	9	US-10-044-692-294	Sequence 294, App
	15	6	100.0	10	9	US-10-044-539-294	Sequence 294, App
	16	6	100.0	10	12	US-10-033-145-56	Sequence 56, Appl
	17	6	100.0	10	12	US-10-033-145-358	Sequence 358, App
	18	6	100.0	10	12	US-10-033-145-613	Sequence 613, App
	19	6	100.0	10	12	US-10-033-145-1694	Sequence 1694, Ap
	20	6	100.0	11	9	US-09-835-370-63	Sequence 63, Appl
	21	6	100.0	11	9	US-10-122-630-5	Sequence 5, Appli
c	22	6	100.0	11	9	US-10-122-630-9	Sequence 9, Appli
	23	6	100.0	11	9	US-10-122-633-5	Sequence 5, Appli
c	24	6	100.0	11	9	US-10-122-633-9	Sequence 9, Appli
c	25	6	100.0	11	9	US-09-249-155-57	Sequence 57, Appl
c	26	6	100.0	11	9	US-09-942-310-7	Sequence 7, Appli
	27	6	100.0	11	9	US-09-942-310-44	Sequence 44, Appl
c	28	6	100.0	11	9	US-10-038-335-9	Sequence 9, Appli
c	29	6	100.0	11	10	US-09-057-351-2	Sequence 2, Appli
c	30	6	100.0	12	8	US-08-463-404-2	Sequence 2, Appli
	31	6	100.0	12	8	US-08-463-404-3	Sequence 3, Appli
c	32	6	100.0	12	8	US-08-463-404-7	Sequence 7, Appli
c	33	6	100.0	12	9	US-10-132-002-1	Sequence 1, Appli
	34	6	100.0	12	9	US-10-132-002-3	Sequence 3, Appli
c	35	6	100.0	12	9	US-10-073-118-18	Sequence 18, Appl
	36	6	100.0	12	9	US-10-117-108A-41	Sequence 41, Appl
c	37	6	100.0	12	9	US-10-117-108A-53	Sequence 53, Appl
	38	6	100.0	12	9	US-09-984-664-11	Sequence 11, Appl
	39	6	100.0	12	10	US-09-057-351-39	Sequence 39, Appl
	40	6	100.0	12	10	US-09-968-355-1	Sequence 1, Appli
	41	6	100.0	12	10	US-09-375-924C-6	Sequence 6, Appli
	42	6	100.0	13	9	US-09-893-252-4	Sequence 4, Appli
	43	6	100.0	13	9	US-10-038-335-1	Sequence 1, Appli
	44	6	100.0	13	9	US-10-038-335-2	Sequence 2, Appli
	45	6	100.0	14	8	US-08-591-486B-123	Sequence 123, App

ALIGNMENTS

RESULT 1
US-10-122-630-11
; Sequence 11, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-11

Query Match 100.0%; Score 6; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA (genomic)
US-08-729-598-8

  Query Match            100.0%;  Score 6;  DB 3;  Length 7;
  Best Local Similarity  100.0%;  Pred. No. 4.1e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
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Db          2 TTAGGG 7


RESULT 15
US-08-838-545-15
; Sequence 15, Application US/08838545
; Patent No. 6046307
;  GENERAL INFORMATION:
;    APPLICANT:  Shay, Jerry W.
;    APPLICANT:  Wright, Woodring E.
;    APPLICANT:  Piatyszek, Mieczyslaw A.
;    APPLICANT:  Corey, David R.
;    APPLICANT:  No. 6046307ton, James C.
;    TITLE OF INVENTION:  Modulation of Mammalian Telomerase by
;    TITLE OF INVENTION:  Peptide Nucleic Acids
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/838,545
;      FILING DATE:  09-APR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,019
;      FILING DATE:  09-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-001610US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "peptide nucleic acid (PNA),
;      DESCRIPTION:  where (deoxy(ribose-phosphate linkages are replaced by
;      DESCRIPTION:  N-(2-aminoethyl)glycine units linked to nucleotide bases via
;      DESCRIPTION:  glycine amino N through a methylenecarbonyl linker"
US-08-838-545-15

  Query Match            100.0%;  Score 6;  DB 3;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 3.6e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          2 TTAGGG 7


Search completed: July  6, 2003, 09:42:20
Job time : 31.0714 secs
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;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-018-545-3

  Query Match             100.0%;  Score 6;  DB 3;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 12
US-09-114-399-3
; Sequence 3, Application US/09114399
; Patent No. 6245747
; GENERAL INFORMATION:
;  APPLICANT:  Porter, Thomas R.
;  APPLICANT:  Iversen, Patrick L.
;  APPLICANT:  Meyer, Gary D.
;  TITLE OF INVENTION:  Targeted Site Specific Drug Delivery
;  TITLE OF INVENTION:  Compositions and Method of Use
;  FILE REFERENCE:  0450-0310.31
;  CURRENT APPLICATION NUMBER: US/09/114,399
;  CURRENT FILING DATE:  1998-07-13
;  PRIOR APPLICATION NUMBER:  US 08/615,495
;  PRIOR FILING DATE:  1996-03-12
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PS-ODN
US-09-114-399-3

  Query Match             100.0%;  Score 6;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 13
PCT-US96-01206-1
; Sequence 1, Application PC/TUS9601206
;  GENERAL INFORMATION:
;    APPLICANT:  Iverson, Patrick L.
;    APPLICANT:  Mata, John E.
;    TITLE OF INVENTION:  Synthetic Oligodeoxynucleotides Which
;    TITLE OF INVENTION:  Mimic Telomeric Sequences for Use in the Treatment of
;    TITLE OF INVENTION:  Cancer and other Diseases
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Zarley, McKee, Thomte, Voorhees & Sease
;      STREET:  801 Grand Avenue Suite 3200
;      CITY:  Des Moines
;      STATE:  Iowa
;      COUNTRY:  United States
;      ZIP:  50309
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/01206
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/381,097
;      FILING DATE:  31-JAN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  NEbel, Heidi S.
;      REGISTRATION NUMBER:  37,719
;      REFERENCE/DOCKET NUMBER:  UNMC# 63092
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  515-288-3667
;      TELEFAX:  515-288-1338
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
PCT-US96-01206-1

  Query Match             100.0%;  Score 6;  DB 5;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 14
US-08-729-598-8
; Sequence 8, Application US/08729598
; Patent No. 6001657
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Charles C.
;    APPLICANT:  Brown II, Bernard A.
;    APPLICANT:  Roberts, John J.
;    APPLICANT:  Pelsue, Stephen A.
;    TITLE OF INVENTION:  Antibodies That Selectively Bind
;    TITLE OF INVENTION:  Quadruplex Nucleic Acids
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sorojini J. Biswas
;      STREET:  P.O. Box 37428
;      CITY:  Raleigh
;      STATE:  No. 6001657th Carolina
;      COUNTRY:  USA
;      ZIP:  27627
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/729,598
;      FILING DATE:  11-OCT-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Biswas, Sorojini J.
;      REGISTRATION NUMBER:  39,111
;      REFERENCE/DOCKET NUMBER:  5051-301A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919) 854-1400
;      TELEFAX:  (919) 854-1401
;  INFORMATION FOR SEQ ID NO:  8:
```

```
;    APPLICANT:  Nam Woo Kim
;    APPLICANT:  Homayoun Vaziri
;    TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF
;    TITLE OF INVENTION:  CONDITIONS RELATED TO
;    TITLE OF INVENTION:  TEOLOMERE LENGTH AND/OR
;    TITLE OF INVENTION:  TELOMERASE ACTIVITY
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,867
;      FILING DATE:  March 14, 1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/153,051
;      FILING DATE:  No. 6007989ember 12, 1993
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Chambers, Daniel M.
;      REGISTRATION NUMBER:  34,561
;      REFERENCE/DOCKET NUMBER:  224/232
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-819-867-27

  Query Match             100.0%;  Score 6;  DB 3;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          6 TTAGGG 1


RESULT 10
US-08-630-019A-1
; Sequence 1, Application US/08630019A
; Patent No. 6015710
;  GENERAL INFORMATION:
;    APPLICANT:  Shay, Jerry W.
;    APPLICANT:  Wright, Woodring E.
;    APPLICANT:  Piatyszek, Mieczyslaw A.
;    APPLICANT:  Corey, David
;    APPLICANT:  No. 6015710ton, James C.
;    TITLE OF INVENTION:  Modulation of Mammalian Telomerase by
;    TITLE OF INVENTION:  Peptide Nucleic Acids
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/630,019A
;      FILING DATE:  09-JUN-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-001600US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "peptide nucleic acid (PNA),
;      DESCRIPTION:  where (deoxy)ribose-phosphate linkages are replaced by
;      DESCRIPTION:  N-(2-aminoethyl)glycine units linked to nucleotide bases via
;      DESCRIPTION:  glycine amino nitrogen through a methylenecarbonyl linker"
US-08-630-019A-1

  Query Match             100.0%;  Score 6;  DB 3;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 11
US-09-018-545-3
; Sequence 3, Application US/09018545
; Patent No. 6087493
;  GENERAL INFORMATION:
;    APPLICANT:  Wheelhouse, Richard T.
;    APPLICANT:  Hurley, Laurence H.
;    TITLE OF INVENTION:  PORPHYRIN COMPOUNDS AS TELOMERASE
;    TITLE OF INVENTION:  INHIBITORS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/018,545
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/037,295
;      FILING DATE:  05-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  UTSB:654
```

```
;    ANTI-SENSE:  YES
US-08-670-999-3

  Query Match             100.0%;  Score 6;  DB 2;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 7
US-08-729-598-4
; Sequence 4, Application US/08729598
; Patent No. 6001657
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Charles C.
;    APPLICANT:  Brown II, Bernard A.
;    APPLICANT:  Roberts, John J.
;    APPLICANT:  Pelsue, Stephen A.
;    TITLE OF INVENTION:  Antibodies That Selectively Bind
;    TITLE OF INVENTION:  Quadruplex Nucleic Acids
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sorojini J. Biswas
;      STREET:  P.O. Box 37428
;      CITY:  Raleigh
;      STATE:  No. 6001657th Carolina
;      COUNTRY:  USA
;      ZIP:  27627
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/729,598
;      FILING DATE:  11-OCT-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Biswas, Sorojini J.
;      REGISTRATION NUMBER:  39,111
;      REFERENCE/DOCKET NUMBER:  5051-301A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919) 854-1400
;      TELEFAX:  (919) 854-1401
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA (genomic)
US-08-729-598-4

  Query Match             100.0%;  Score 6;  DB 3;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 8
US-08-819-867-9
; Sequence 9, Application US/08819867
; Patent No. 6007989
;  GENERAL INFORMATION:
;    APPLICANT:  Michael D. West
;    APPLICANT:  Calvin B. Harley
;    APPLICANT:  Scott L. Weinrich
;    APPLICANT:  Catherine M. Strahl
;    APPLICANT:  Michael J. Mceachern
;    APPLICANT:  Jerry Shay
;    APPLICANT:  Woodring E. Wright
;    APPLICANT:  Elizabeth H. Blackburn
;    APPLICANT:  Nam Woo Kim
;    APPLICANT:  Homayoun Vaziri
;    TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF
;    TITLE OF INVENTION:  CONDITIONS RELATED TO
;    TITLE OF INVENTION:  TEOLOMERE LENGTH AND/OR
;    TITLE OF INVENTION:  TELOMERASE ACTIVITY
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,867
;      FILING DATE:  March 14, 1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/153,051
;      FILING DATE:  No. 6007989ember 12, 1993
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Chambers, Daniel M.
;      REGISTRATION NUMBER:  34,561
;      REFERENCE/DOCKET NUMBER:  224/232
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-819-867-9

  Query Match             100.0%;  Score 6;  DB 3;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 9
US-08-819-867-27/c
; Sequence 27, Application US/08819867
; Patent No. 6007989
;  GENERAL INFORMATION:
;    APPLICANT:  Michael D. West
;    APPLICANT:  Calvin B. Harley
;    APPLICANT:  Scott L. Weinrich
;    APPLICANT:  Catherine M. Strahl
;    APPLICANT:  Michael J. Mceachern
;    APPLICANT:  Jerry Shay
;    APPLICANT:  Woodring E. Wright
;    APPLICANT:  Elizabeth H. Blackburn
```

```
;       SOFTWARE:  Word Perfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/337,684
;       FILING DATE:  No. 5686306ember 10, 1994
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/151,477
;       FILING DATE:  No. 5686306ember 12, 1993
;       APPLICATION NUMBER:  08/153,051
;       FILING DATE:  No. 5686306ember 12, 1993
;       APPLICATION NUMBER:  08/060,952
;       FILING DATE:  May 13, 1993
;       APPLICATION NUMBER:  08/038,766
;       FILING DATE:  March 24, 1993
;       APPLICATION NUMBER:  07/882,438
;       FILING DATE:  May 13, 1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warburg, Richard J.
;       REGISTRATION NUMBER:  32,327
;       REFERENCE/DOCKET NUMBER:  210/085
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  6 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-337-684-2

  Query Match             100.0%;  Score 6;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          1 TTAGGG 6


RESULT 5
US-08-151-477A-4/c
; Sequence 4, Application US/08151477A
; Patent No. 5830644
;  GENERAL INFORMATION:
;    APPLICANT:  Michael D. West
;    APPLICANT:  Jerry W. Shay
;    APPLICANT:  Woodring E. Wright
;    APPLICANT:  Elizabeth Blackburn
;    APPLICANT:  Nam Woo Kim
;    APPLICANT:  Calvin B. Harley
;    APPLICANT:  Scott L. Weinrich
;    APPLICANT:  Catherine Strahl
;    APPLICANT:  Michael J. McEachern
;    APPLICANT:  Homayoun Vaziri
;    TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF
;    TITLE OF INVENTION:  CONDITIONS RELATED TO TELEOMERE
;    TITLE OF INVENTION:  LENGTH AND/OR TELOMERASE ACTIVITY
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/151,477A
;      FILING DATE:  No. 5830644ember 12, 1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/038,766
;      FILING DATE:  March 24, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  202/189
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-151-477A-4

  Query Match             100.0%;  Score 6;  DB 2;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          6 TTAGGG 1


RESULT 6
US-08-670-999-3
; Sequence 3, Application US/08670999
; Patent No. 5849727
;  GENERAL INFORMATION:
;    APPLICANT:  Porter, Thomas R.
;    APPLICANT:  Iverson, Patrick L.
;    TITLE OF INVENTION:  Compositions and Methods for Altering
;    TITLE OF INVENTION:  the Biodistribution of Biological Agents
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Zarley, McKee, Thomte, Voorhees & Sease
;      STREET:  801 Grand Suite 3200
;      CITY:  Des Moines
;      STATE:  Iowa
;      COUNTRY:  United States
;      ZIP:  50309
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/670,999
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nebel, Heidi S.
;      REGISTRATION NUMBER:  37,719
;      REFERENCE/DOCKET NUMBER:  unmc 107A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  515-288-3667
;      TELEFAX:  515-288-1338
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
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                    ||||||
Db          1 TTAGGG 6


RESULT 2
US-08-381-097A-5/c
; Sequence 5, Application US/08381097A
; Patent No. 5643890
;  GENERAL INFORMATION:
;    APPLICANT:  Iverson, Patrick L.
;    APPLICANT:  Mata, John E.
;    TITLE OF INVENTION:  Synthteic Oligodeoxyribonucleotides
;    TITLE OF INVENTION:  Which Mimic Telomeric Sequences for Use in the Treatment
;    TITLE OF INVENTION:  of Cancer and Other Diseases
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Zarely, McKee, Thomte, Voorhees, & Sease
;      STREET:  801 Grand Suite 3200
;      CITY:  Des Moines
;      STATE:  Iowa
;      COUNTRY:  United States
;      ZIP:  50309
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/381,097A
;      FILING DATE:  31-JAN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  NEbel, Heidi S
;      REGISTRATION NUMBER:  37,719
;      REFERENCE/DOCKET NUMBER:  unmc 63092
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  515-288-3667
;      TELEFAX:  515-288-1338
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-381-097A-5

  Query Match             100.0%;  Score 6;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          6 TTAGGG 1


RESULT 3
US-08-153-051B-4/c
; Sequence 4, Application US/08153051B
; Patent No. 5645986
;  GENERAL INFORMATION:
;    APPLICANT:  Michael D. West
;    APPLICANT:  Jerry W. Shay
;    APPLICANT:  Woodring E. Wright
;    APPLICANT:  Elizabeth Blackburn
;    APPLICANT:  Nam Woo Kim
;    APPLICANT:  Calvin B. Harley
;    APPLICANT:  Scott L. Weinrich
;    APPLICANT:  Catherine Strahl
;    APPLICANT:  Michael J. McEachern
;    APPLICANT:  Homayoun Vaziri
;    TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF
;    TITLE OF INVENTION:  CONDITIONS RELATED TO TELEOMERE
;    TITLE OF INVENTION:  LENGTH AND/OR TELOMERASE ACTIVITY
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/153,051B
;      FILING DATE:  No. 5645986ember 12, 1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/038,766
;      FILING DATE:  March 24, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  204/195
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-153-051B-4

  Query Match             100.0%;  Score 6;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          6 TTAGGG 1


RESULT 4
US-08-337-684-2
; Sequence 2, Application US/08337684
; Patent No. 5686306
;  GENERAL INFORMATION:
;    APPLICANT:  West, Michael David
;    APPLICANT:  Shay, Jerry
;    APPLICANT:  Wright, Woodring E.
;    TITLE OF INVENTION:  METHODS AND REAGENTS FOR
;    TITLE OF INVENTION:  MEASURING TELOMERES
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 07:52:05 ; Search time 31.0714 Seconds
(without alignments)
59.220 Million cell updates/sec

Title: US-09-540-843-11
Perfect score: 6
Sequence: 1 ttaggg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 558892

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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c	2	6	100.0	6	1	US-08-381-097A-5	Sequence 5, Appli
c	3	6	100.0	6	1	US-08-153-051B-4	Sequence 4, Appli
	4	6	100.0	6	1	US-08-337-684-2	Sequence 2, Appli
c	5	6	100.0	6	2	US-08-151-477A-4	Sequence 4, Appli
	6	6	100.0	6	2	US-08-670-999-3	Sequence 3, Appli
	7	6	100.0	6	3	US-08-729-598-4	Sequence 4, Appli
	8	6	100.0	6	3	US-08-819-867-9	Sequence 9, Appli
c	9	6	100.0	6	3	US-08-819-867-27	Sequence 27, Appl
	10	6	100.0	6	3	US-08-630-019A-1	Sequence 1, Appli
	11	6	100.0	6	3	US-09-018-545-3	Sequence 3, Appli
	12	6	100.0	6	4	US-09-114-399-3	Sequence 3, Appli
	13	6	100.0	6	5	PCT-US96-01206-1	Sequence 1, Appli
	14	6	100.0	7	3	US-08-729-598-8	Sequence 8, Appli
	15	6	100.0	8	3	US-08-838-545-15	Sequence 15, Appl
c	16	6	100.0	8	3	US-08-838-545-30	Sequence 30, Appl
	17	6	100.0	8	3	US-08-838-545-34	Sequence 34, Appl
	18	6	100.0	8	4	US-09-349-532-15	Sequence 15, Appl
c	19	6	100.0	8	4	US-09-349-532-30	Sequence 30, Appl
	20	6	100.0	8	4	US-09-349-532-34	Sequence 34, Appl
	21	6	100.0	9	1	US-08-337-684-3	Sequence 3, Appli
	22	6	100.0	9	3	US-08-630-019A-27	Sequence 27, Appl
	23	6	100.0	9	3	US-09-069-434-14	Sequence 14, Appl
	24	6	100.0	9	3	US-08-838-545-16	Sequence 16, Appl
	25	6	100.0	9	4	US-09-349-532-16	Sequence 16, Appl
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	27	6	100.0	10	2	US-08-531-743-10	Sequence 10, Appl
	28	6	100.0	10	3	US-08-630-019A-8	Sequence 8, Appli
	29	6	100.0	10	3	US-08-838-545-7	Sequence 7, Appli
c	30	6	100.0	10	3	US-08-838-545-11	Sequence 11, Appl
	31	6	100.0	10	3	US-08-838-545-17	Sequence 17, Appl
	32	6	100.0	10	3	US-08-838-545-21	Sequence 21, Appl
c	33	6	100.0	10	3	US-08-838-545-29	Sequence 29, Appl
	34	6	100.0	10	4	US-08-974-549A-527	Sequence 527, App
	35	6	100.0	10	4	US-09-349-532-7	Sequence 7, Appli
c	36	6	100.0	10	4	US-09-349-532-11	Sequence 11, Appl
	37	6	100.0	10	4	US-09-349-532-17	Sequence 17, Appl
	38	6	100.0	10	4	US-09-349-532-21	Sequence 21, Appl
c	39	6	100.0	10	4	US-09-349-532-29	Sequence 29, Appl
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	43	6	100.0	11	2	US-08-531-743-11	Sequence 11, Appl
c	44	6	100.0	11	2	US-08-531-743-12	Sequence 12, Appl
c	45	6	100.0	11	2	US-08-485-778-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08-381-097A-3
; Sequence 3, Application US/08381097A
; Patent No. 5643890
; GENERAL INFORMATION:
; APPLICANT: Iverson, Patrick L.
; APPLICANT: Mata, John E.
; TITLE OF INVENTION: Synthteic Oligodeoxyribonucleotides
; TITLE OF INVENTION: Which Mimic Telomeric Sequences for Use in the Treatment
; TITLE OF INVENTION: of Cancer and Other Diseases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zarely, McKee, Thomte, Voorhees, & Sease
; STREET: 801 Grand Suite 3200
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: United States
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,097A
; FILING DATE: 31-JAN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: NEbel, Heidi S
; REGISTRATION NUMBER: 37,719
; REFERENCE/DOCKET NUMBER: unmc 63092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 515-288-3667
; TELEFAX: 515-288-1338
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-381-097A-3

Query Match 100.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6

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REFERENCE   1  (bases 1 to 21)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821108.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 10
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 21 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM5  row: P  column: 5
            High quality sequence stop: 10.
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                     /clone="IMAGE:2821108"
                     /clone_lib="NIH_MGC_7"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT        4 a      6 c      0 g     11 t
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  Best Local Similarity  100.0%;  Pred. No. 4.5e+05;
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Qy          1 TTAGGG 6
              ||||||
Db         20 TTAGGG 15
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RESULT 15
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LOCUS       AZ331625                 21 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0059M07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0059M07 R, DNA sequence.
ACCESSION   AZ331625
VERSION     AZ331625.1  GI:10394498
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0059  row: M  column: 07
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
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                     /db_xref="taxon:10090"
                     /clone="UUGC1M0059M07"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        8 a      7 c      0 g      6 t
ORIGIN
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  Query Match           100.0%;  Score 6;  DB 17;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 4.5e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db         16 TTAGGG 11


Search completed: July  6, 2003, 09:39:51
Job time : 898.643 secs
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                     /strain="TREU927"
                     /db_xref="taxon:5691"
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BASE COUNT        6 a      11 c       0 g       3 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 17;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db         19 TTAGGG 14


RESULT 12
TA199G02Q/c
LOCUS       TA199G02Q                 20 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 199g02, reverse sequence,
            genomic survey sequence.
ACCESSION   AL476798
VERSION     AL476798.1  GI:11843362
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Trypanosoma brucei"
                     /strain="TREU927"
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ORIGIN

  Query Match             100.0%;  Score 6;  DB 17;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db         20 TTAGGG 15


RESULT 13
AW248826/c
LOCUS       AW248826                  21 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821056.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821056 3',
            mRNA sequence.
ACCESSION   AW248826
VERSION     AW248826.1  GI:6591819
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821056.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 21
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 21 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM5  row: N  column: 1
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821056"
                     /clone_lib="NIH_MGC_7"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT        4 a       3 c       3 g      11 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 10;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
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Db         20 TTAGGG 15


RESULT 14
AW248836/c
LOCUS       AW248836                  21 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821108.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821108 3',
            mRNA sequence.
ACCESSION   AW248836
VERSION     AW248836.1  GI:6591829
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0071D09"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 2 a 2 c 10 g 6 t
ORIGIN

Query Match 100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
||||||
Db 6 TTAGGG 11

RESULT 10
AZ960008/c
LOCUS AZ960008 20 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0227G21R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0227G21 R, DNA sequence.
ACCESSION AZ960008
VERSION AZ960008.1 GI:13831235
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0227 row: G column: 21
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0227G21"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 8 a 5 c 2 g 5 t
ORIGIN

Query Match 100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
||||||
Db 18 TTAGGG 13

RESULT 11
TA158A03P/c
LOCUS TA158A03P 20 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 158a03, forward sequence, genomic survey sequence.
ACCESSION AL472050
VERSION AL472050.1 GI:11837404
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 20)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES Location/Qualifiers
source 1. .20

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0467O10"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 5 a 2 c 7 g 6 t
ORIGIN

Query Match 100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
||||||
Db 13 TTAGGG 18

RESULT 8
AZ662909
LOCUS AZ662909 20 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0542G17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0542G17 F, DNA sequence.
ACCESSION AZ662909
VERSION AZ662909.1 GI:11800055
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0542 row: G column: 17
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0542G17"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 2 a 2 c 11 g 5 t
ORIGIN

Query Match 100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
||||||
Db 7 TTAGGG 12

RESULT 9
AZ808291
LOCUS AZ808291 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0071D09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0071D09 R, DNA sequence.
ACCESSION AZ808291
VERSION AZ808291.1 GI:12973320
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0071 row: D column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0102N07"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 8 a 6 c 2 g 3 t
ORIGIN

Query Match 100.0%; Score 6; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
||||||
Db 17 TTAGGG 12

RESULT 6
AZ345513/c
LOCUS AZ345513 20 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0080J04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080J04 F, DNA sequence.
ACCESSION AZ345513
VERSION AZ345513.1 GI:10424750
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: J column: 04
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080J04"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 13 c 0 g 4 t
ORIGIN

Query Match 100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
||||||
Db 16 TTAGGG 11

RESULT 7
AZ627174
LOCUS AZ627174 20 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0467O10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0467O10 R, DNA sequence.
ACCESSION AZ627174
VERSION AZ627174.1 GI:11749364
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0467 row: O column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0200F10"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 5 c 2 g 5 t
ORIGIN

Query Match 100.0%; Score 6; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
||||||
Db 8 TTAGGG 3

RESULT 4
AZ614760
LOCUS AZ614760 19 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0443A17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0443A17 R, DNA sequence.
ACCESSION AZ614760
VERSION AZ614760.1 GI:11736950
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0443 row: A column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0443A17"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 0 c 10 g 6 t
ORIGIN

Query Match 100.0%; Score 6; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
||||||
Db 4 TTAGGG 9

RESULT 5
AZ826736/c
LOCUS AZ826736 19 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0102N07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0102N07 R, DNA sequence.
ACCESSION AZ826736
VERSION AZ826736.1 GI:12996644
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0102 row: N column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19

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            http://www.genome.washington.edu Low Quality Sequence: 15
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 16 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM1  row: K  column: 7
            High quality sequence stop: 15.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2819454"
                      /clone_lib="NIH_MGC_7"
                      /tissue_type="small cell carcinoma"
                      /cell_line="MGC3"
                      /lab_host="DH10B (phage-resistant)"
                      /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                      EcoRI; cDNA made by oligo-dT priming.  Directionally
                      cloned into EcoRI/XhoI sites using the following 5'
                      adaptor: GGCACGAG(G).  Size-selected >500bp for average
                      insert size 1.8kb.  Library constructed by Ling Hong in
                      the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT        3 a      0 c      3 g     10 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 10;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
              ||||||
Db          9 TTAGGG 14


RESULT 2
AZ392246
LOCUS       AZ392246                 19 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0154G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0154G12 R, DNA sequence.
ACCESSION   AZ392246
VERSION     AZ392246.1  GI:10507234
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0154  row: G  column: 12
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0154G12"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
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                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT        3 a      5 c      5 g     6 t
ORIGIN

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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGGG 6
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Db         14 TTAGGG 19


RESULT 3
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LOCUS       AZ422271                 19 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0200F10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0200F10 R, DNA sequence.
ACCESSION   AZ422271
VERSION     AZ422271.1  GI:10546284
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0200  row: F  column: 10
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Title: US-09-540-843-11
Perfect score: 6
Sequence: 1 ttaggg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 60474

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
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8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
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17: gb_gss:*
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22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	6	100.0	16	10	AW248958	AW248958 2819454.3
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c	3	6	100.0	19	17	AZ422271	AZ422271 1M0200F10
	4	6	100.0	19	17	AZ614760	AZ614760 1M0443A17
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	7	6	100.0	20	17	AZ627174	AZ627174 1M0467O10
	8	6	100.0	20	17	AZ662909	AZ662909 1M0542G17
	9	6	100.0	20	17	AZ808291	AZ808291 2M0071D09
c	10	6	100.0	20	17	AZ960008	AZ960008 2M0227G21
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c	13	6	100.0	21	10	AW248826	AW248826 2821056.3
c	14	6	100.0	21	10	AW248836	AW248836 2821108.3
c	15	6	100.0	21	17	AZ331625	AZ331625 1M0059M07
c	16	6	100.0	21	17	AZ399400	AZ399400 1M0165C13
c	17	6	100.0	21	17	AZ445481	AZ445481 1M0241P15
c	18	6	100.0	21	17	AZ626594	AZ626594 1M0466J20
c	19	6	100.0	21	17	AZ760907	AZ760907 1M0554P21
	20	6	100.0	21	17	AZ766315	AZ766315 1M0563K14
c	21	6	100.0	21	17	AZ828389	AZ828389 2M0105P16
c	22	6	100.0	21	17	AZ833919	AZ833919 2M0116N18
c	23	6	100.0	21	17	AZ877328	AZ877328 2M0192C18
c	24	6	100.0	22	9	AA954126	AA954126 oq66a07.s
	25	6	100.0	22	9	AA527213	AA527213 ni27b11.s
c	26	6	100.0	22	14	D18745	D18745 MUSGS01807
c	27	6	100.0	22	17	AZ324747	AZ324747 1M0046O13
c	28	6	100.0	22	17	AZ464647	AZ464647 1M0274D09
	29	6	100.0	22	17	AZ483833	AZ483833 1M0310H03
	30	6	100.0	22	17	AZ500414	AZ500414 1M0338G17
c	31	6	100.0	22	17	AZ598320	AZ598320 1M0413N04
c	32	6	100.0	22	17	AZ629501	AZ629501 1M0482G06
	33	6	100.0	22	17	AZ666649	AZ666649 1M0548M19
	34	6	100.0	22	17	AZ836104	AZ836104 2M0130C17
c	35	6	100.0	22	17	AZ855118	AZ855118 2M0159H05
c	36	6	100.0	23	9	AU258772	AU258772 AU258772
c	37	6	100.0	23	17	AZ423815	AZ423815 1M0203O23
	38	6	100.0	23	17	AZ465280	AZ465280 1M0275A10
	39	6	100.0	23	17	AZ623979	AZ623979 1M0462E14
	40	6	100.0	23	17	AZ817008	AZ817008 2M0086E02
c	41	6	100.0	23	17	AZ979817	AZ979817 2M0256F09
	42	6	100.0	23	17	BH857265	BH857265 SALK_0765
c	43	6	100.0	24	17	AZ309633	AZ309633 1M0016B22
	44	6	100.0	24	17	AZ785628	AZ785628 2M0029M09
	45	6	100.0	24	17	AZ806300	AZ806300 2M0068F13

ALIGNMENTS

RESULT 1
AW248958
LOCUS AW248958 16 bp mRNA linear EST 07-JAN-2000
DEFINITION 2819454.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819454 3', mRNA sequence.
ACCESSION AW248958
VERSION AW248958.1 GI:6591951
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 16)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2819454.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center:

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Db          6 CCCTAA 1


RESULT 14
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LOCUS       AR016034                  11 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 2 from patent US 5776679.
ACCESSION   AR016034
VERSION     AR016034.1  GI:3972311
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
  TITLE     Assays for the DNA component of human telomerase
  JOURNAL   Patent: US 5776679-A 2 07-JUL-1998;
FEATURES             Location/Qualifiers
     source          1. .11
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Qy          1 CCCTAA 6
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Db          5 CCCTAA 10


RESULT 15
AR026486/c
LOCUS       AR026486                  11 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 11 from patent US 5856096.
ACCESSION   AR026486
VERSION     AR026486.1  GI:5937326
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Windle,B.E., Qiu,M., Chen,S.-F., Fletcher,T.M. and Maine,I.
  TITLE     Rapid and sensitive assays for detecting and distinguishing between
            processive and non-processive telomerase activities
  JOURNAL   Patent: US 5856096-A 11 05-JAN-1999;
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ORIGIN

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Qy          1 CCCTAA 6
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Db          7 CCCTAA 2


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Qy          1 CCCTAA 6
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RESULT 11
AX153524/c
LOCUS       AX153524                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1439 from Patent WO0138577.
ACCESSION   AX153524
VERSION     AX153524.1  GI:14535175
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1439 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
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Qy          1 CCCTAA 6
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Db         10 CCCTAA 5


RESULT 12
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LOCUS       BD011231                 10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Human telomerase catalytic subunit.
ACCESSION   BD011231
VERSION     BD011231.1  GI:18639604
KEYWORDS    JP 2001081042-A/188.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
            Harley,C.B. and Andrews,W.H.
  TITLE     Human telomerase catalytic subunit
  JOURNAL   Patent: JP 2001081042-A 188 27-MAR-2001;
            GERON CORP,UNIVERSITY TECHNOLOGY CORP
COMMENT     OS   Unidentified
            PN   JP 2001081042-A/188
            PD   27-MAR-2001
            PF   27-JUL-2000 JP 2000227474
            PR   01-OCT-1996 US    08/724643,18-APR-1997 US    08/844419 PR
            25-APR-1997 US    08/846017,06-MAY-1997 US    08/851843 PR
            09-MAY-1997 US    08/854050,14-AUG-1997 US    08/911312 PR
            14-AUG-1997 US    08/912951,14-AUG-1997 US    08/915503 PI   THOMAS
            R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI   GREG B
            MORIN,
            PI   CALVIN B HARLEY,WILLIAM H ANDREWS
            PC   A61K38/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00,A61P43/00,
            PC   C07K5/10,
            PC   C07K5/107,C07K5/117,C07K7/06,C07K7/08,C07K16/40,C12N9/12, PC
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            CC   Topology: Linear;
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Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 13
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LOCUS       E36980                   10 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Human telomerase catalytic subunit promoter.
ACCESSION   E36980
VERSION     E36980.1  GI:13022943
KEYWORDS    JP 1999253177-A/188.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
            Calvin,B.H. and William,H.A.
  TITLE     Human telomerase catalytic subunit promoter
  JOURNAL   Patent: JP 1999253177-A 188 21-SEP-1999;
            JERON CORP,UNIVERSITY TECHNOLOGY CORP
COMMENT     OS   Unidentified
            PN   JP 1999253177-A/188
            PD   21-SEP-1999
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            PR   01-OCT-1996 US   08/724.643,18-APR-1997 US   08/844.419, PR
            25-APR-1997 US   08/846.017,06-MAY-1997 US   08/851.843, PR
            09-MAY-1997 US   08/854.050,14-AUG-1997 US   08/911.312, PR
            14-AUG-1997 US   08/912.951,14-AUG-1997 US   08/915.503 PI   THOMAS
            R SECHI,JOCHIMU RINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI   GREG B
            MORIN,
            PI   CALVIN B HAREI,WILLIAM H ANDREWS
            PC   C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,
            PC   C12Q1/02,
            PC   C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC
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            PC   C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,(C12N1/19, PC
            C12R1:84),
            PC   (C12N1/21,C12R1:19),(C12N9/12,C12R1:19),(C12N9/12,C12R1:84),
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DEFINITION  Sequence 10 from patent US 5856096.
ACCESSION   AR026485
VERSION     AR026485.1  GI:5937325
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Windle,B.E., Qiu,M., Chen,S.-F., Fletcher,T.M. and Maine,I.
  TITLE     Rapid and sensitive assays for detecting and distinguishing between
            processive and non-processive telomerase activities
  JOURNAL   Patent: US 5856096-A 10 05-JAN-1999;
FEATURES             Location/Qualifiers
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Db          6 CCCTAA 1


RESULT 7
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LOCUS       AX152177                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 92 from Patent WO0138577.
ACCESSION   AX152177
VERSION     AX152177.1  GI:14533828
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 92 31-MAY-2001;
            The Johns Hopkins University (US)
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Qy          1 CCCTAA 6
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Db          7 CCCTAA 2


RESULT 8
AX153381
LOCUS       AX153381                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1296 from Patent WO0138577.
ACCESSION   AX153381
VERSION     AX153381.1  GI:14535032
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1296 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          3 CCCTAA 8


RESULT 9
AX153382
LOCUS       AX153382                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1297 from Patent WO0138577.
ACCESSION   AX153382
VERSION     AX153382.1  GI:14535033
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1297 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      3 c      0 g      2 t
ORIGIN

  Query Match           100.0%;  Score 6;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 3.9e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          3 CCCTAA 8


RESULT 10
AX153383
LOCUS       AX153383                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1298 from Patent WO0138577.
ACCESSION   AX153383
VERSION     AX153383.1  GI:14535034
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1298 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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          CANCER INSTITUTE, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="synthetic primer"
BASE COUNT        2 a      3 c      0 g      1 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 4.8e+09;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          1 CCCTAA 6


RESULT 2
AX058275/c
LOCUS       AX058275                  6 bp    DNA     linear   PAT 17-JAN-2001
DEFINITION  Sequence 10 from Patent WO0074667.
ACCESSION   AX058275
VERSION     AX058275.1  GI:12310774
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Au,J.L. and Wientjes,G.
  TITLE     Compositions active in telomere damage comprising a taxane and
            telomerase inhibitor
  JOURNAL   Patent: WO 0074667-A 10 14-DEC-2000;
            Au, Jessie L.S. (US) ; Wientjes, Guillaume (US)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="primer/probe"
BASE COUNT        1 a      0 c      3 g      2 t
ORIGIN

  Query Match            100.0%;  Score 6;  DB 6;  Length 6;
  Best Local Similarity  100.0%;  Pred. No. 4.8e+09;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 3
AX175285/c
LOCUS       AX175285                  6 bp    DNA     linear   PAT 03-JUL-2001
DEFINITION  Sequence 49 from Patent WO0144465.
ACCESSION   AX175285
VERSION     AX175285.1  GI:14598653
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Phillips,N.C. and Filion,M.C.
  TITLE     Therapeutically useful synthetic oligonucleotides
  JOURNAL   Patent: WO 0144465-A 49 21-JUN-2001;
            Bioniche Life Sciences Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        1 a      0 c      3 g      2 t
ORIGIN
```

```
  Query Match            100.0%;  Score 6;  DB 6;  Length 6;
  Best Local Similarity  100.0%;  Pred. No. 4.8e+09;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 4
AX268763/c
LOCUS       AX268763                  6 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 11 from Patent WO0174342.
ACCESSION   AX268763
VERSION     AX268763.1  GI:16541835
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gilchrest,B.A., Yaar,M. and Eller,M.
  TITLE     Use of locally applied dna fragments
  JOURNAL   Patent: WO 0174342-A 11 11-OCT-2001;
            TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA Fragment"
BASE COUNT        1 a      0 c      3 g      2 t
ORIGIN

  Query Match            100.0%;  Score 6;  DB 6;  Length 6;
  Best Local Similarity  100.0%;  Pred. No. 4.8e+09;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 5
AX268764
LOCUS       AX268764                  6 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 12 from Patent WO0174342.
ACCESSION   AX268764
VERSION     AX268764.1  GI:16541836
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gilchrest,B.A., Yaar,M. and Eller,M.
  TITLE     Use of locally applied dna fragments
  JOURNAL   Patent: WO 0174342-A 12 11-OCT-2001;
            TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA Fragment"
BASE COUNT        2 a      3 c      0 g      1 t
ORIGIN

  Query Match            100.0%;  Score 6;  DB 6;  Length 6;
  Best Local Similarity  100.0%;  Pred. No. 4.8e+09;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          1 CCCTAA 6
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 06:42:31 ; Search time 285 Seconds
(without alignments)
612.691 Million cell updates/sec

Title: US-09-540-843-12
Perfect score: 6
Sequence: 1 ccctaa 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 774614

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
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26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	6	100.0	6	6	AX055801	AX055801 Sequence
c	2	6	100.0	6	6	AX058275	AX058275 Sequence
c	3	6	100.0	6	6	AX175285	AX175285 Sequence
c	4	6	100.0	6	6	AX268763	AX268763 Sequence
	5	6	100.0	6	6	AX268764	AX268764 Sequence
c	6	6	100.0	10	6	AR026485	AR026485 Sequence
c	7	6	100.0	10	6	AX152177	AX152177 Sequence
	8	6	100.0	10	6	AX153381	AX153381 Sequence
	9	6	100.0	10	6	AX153382	AX153382 Sequence
	10	6	100.0	10	6	AX153383	AX153383 Sequence
c	11	6	100.0	10	6	AX153524	AX153524 Sequence
c	12	6	100.0	10	6	BD011231	BD011231 Human tel
c	13	6	100.0	10	6	E36980	E36980 Human telom
	14	6	100.0	11	6	AR016034	AR016034 Sequence
c	15	6	100.0	11	6	AR026486	AR026486 Sequence
	16	6	100.0	11	6	AR026487	AR026487 Sequence
	17	6	100.0	11	6	AR059195	AR059195 Sequence
	18	6	100.0	11	6	AR075506	AR075506 Sequence
	19	6	100.0	11	6	AR161904	AR161904 Sequence
	20	6	100.0	11	6	AX033373	AX033373 Sequence
c	21	6	100.0	11	6	AX268757	AX268757 Sequence
	22	6	100.0	11	6	AX268761	AX268761 Sequence
c	23	6	100.0	11	6	AX283296	AX283296 Sequence
	24	6	100.0	11	6	AX394462	AX394462 Sequence
c	25	6	100.0	11	6	AX394499	AX394499 Sequence
c	26	6	100.0	11	6	AX471710	AX471710 Sequence
	27	6	100.0	11	6	BD003369	BD003369 Mammalian
	28	6	100.0	11	6	I31749	I31749 Sequence 2
	29	6	100.0	12	6	A21302	A21302 Nucleotide
c	30	6	100.0	12	6	AR026476	AR026476 Sequence
	31	6	100.0	12	6	AR026477	AR026477 Sequence
	32	6	100.0	12	6	AR026480	AR026480 Sequence
	33	6	100.0	12	6	AR050933	AR050933 Sequence
c	34	6	100.0	12	6	AR050934	AR050934 Sequence
	35	6	100.0	12	6	AR050938	AR050938 Sequence
c	36	6	100.0	12	6	AR059223	AR059223 Sequence
	37	6	100.0	12	6	AR059544	AR059544 Sequence
c	38	6	100.0	12	6	AR059545	AR059545 Sequence
c	39	6	100.0	12	6	AR075547	AR075547 Sequence
	40	6	100.0	12	6	AR134878	AR134878 Sequence
c	41	6	100.0	12	6	AR134879	AR134879 Sequence
	42	6	100.0	12	6	AR199363	AR199363 Sequence
c	43	6	100.0	12	6	AR200885	AR200885 Sequence
	44	6	100.0	12	6	AR204552	AR204552 Sequence
c	45	6	100.0	12	6	AR204553	AR204553 Sequence

ALIGNMENTS

RESULT 1
AX055801
LOCUS AX055801 6 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 5 from Patent WO0073420.
ACCESSION AX055801
VERSION AX055801.1 GI:12228914
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 6)
AUTHORS Hahn,W.C. and Weinberg,R.A.
TITLE Creation of human tumorigenic cells and uses therefor
JOURNAL Patent: WO 0073420-A 5 07-DEC-2000;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; DANA-FARBER

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Qy          1 CCCTAA 6
              ||||||
Db          7 CCCTAA 2


RESULT 14
AAT05735/c
ID   AAT05735 standard; DNA; 9 BP.
XX
AC   AAT05735;
XX
DT   01-FEB-1996  (first entry)
XX
DE   Telomerase oligonucleotide substrate #2.
XX
KW   Telomerase; proliferation; telomere; hybrid; immortalised cell; anaemia;
KW   transplantation; cell therapy; treatment; AIDS; leukaemia; lymphoma; ss.
XX
OS   Synthetic.
XX
PN   WO9513383-A1.
XX
PD   18-MAY-1995.
XX
PF   10-NOV-1994;   94WO-US13130.
XX
PR   12-NOV-1993;   93US-0153051.
PR   12-NOV-1993;   93US-0151477.
XX
PA   (GERO-) GERON CORP.
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Shay J,  West MD,  Wright WE;
XX
DR   WPI; 1995-224051/29.
XX
PT   Increasing telomere length in cells  - to increase proliferative
PT   capacity and therefore delay cellular senescence, useful in cell
PT   therapy and transplantation
XX
PS   Claim 12; Page 29; 38pp; English.
XX
CC   Oligonucleotides AAT05734-7 are examples of telomerase substrates used
CC   to increase the proliferative capacity of normal cells that express
CC   telomerase activity.  The oligonucleotides allow an increase in
CC   length of telomeres in normal cells and in hybrids of normal and
CC   immortalised cells.  The increase in telomere length extends the
CC   capacity of cells to replicate, esp. those treated ex vivo and used
CC   for transplantation techniques e.g. cell therapy, for the treatment
CC   of AIDS, anaemia, leukaemia or lymphoma.
XX
SQ   Sequence 9 BP; 2 A; 0 C; 3 G; 4 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 16;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 15
AAT89240/c
ID   AAT89240 standard; DNA; 9 BP.
XX
AC   AAT89240;
XX
DT   12-MAY-1998  (first entry)
XX
DE   Peptide nucleic acid 15, targeted to mammalian telomerase.
XX
KW   Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
KW   inhibitor; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..9
FT                   /*tag= a
FT                   /note= "Sugar-phosphate backbone has been replaced by
FT                         a peptide backbone"
XX
PN   WO9738013-A1.
XX
PD   16-OCT-1997.
XX
PF   09-APR-1997;   97WO-US05931.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (GERO-) GERON CORP.
XX
PI   Corey D,  Norton JC,  Piatyszek MA,  Shay JW,  Wright WE;
XX
DR   WPI; 1997-512647/47.
XX
PT   New peptide nucleic acids hybridising to mammalian telomerase RNA -
PT   used to inhibit telomerase, for treating tumours and other
PT   proliferative diseases, also for diagnosis
XX
PS   Claim 9; Page 59; 76pp; English.
XX
CC   This sequence is a novel peptide nucleic acid (PNA), which acts as
CC   an inhibitor of mammalian, preferably human, telomerase.  The PNAs
CC   hybridise specifically to an RNA component of mammalian telomerase,
CC   and include the sequence GGG for specific hybridisation to the template
CC   region of this component.  PNAs can be used as probes to detect the
CC   RNA component of mammalian telomerase and as inhibitors of telomerase
CC   activity, especially in the treatment of cancer.
XX
SQ   Sequence 9 BP; 2 A; 0 C; 4 G; 3 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 18;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          8 CCCTAA 3


Search completed: July  6, 2003, 08:07:24
Job time : 133.107 secs
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OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..8
FT                   /*tag= a
FT                   /note= "This sequence is a peptide nucleic acid, i.e. it
FT                          contains a polyamide backbone instead of a
FT                          deoxyribose backbone"
XX
PN   US6294650-B1.
XX
PD   25-SEP-2001.
XX
PF   08-JUL-1999;   99US-0349532.
XX
PR   09-APR-1997;   97US-0838545.
PR   09-APR-1996;   96US-0630019.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Shay JW,  Wright WE,  Piatyszek MA,  Corey DR,  Norton JC;
XX
DR   WPI; 2001-638024/73.
XX
PT   New peptide nucleic acids that hybridises to the RNA component of
PT   mammalian telomerase, useful for treating or preventing cancer,
PT   inflammation, lymphoproliferative diseases, autoimmune disease, or
PT   neurodegenerative diseases  -
XX
PS   Claim 7; Column 73; 46pp; English.
XX
CC   The present invention relates to peptide nucleic acids (PNAs), comprising
CC   a sequence of 6-25 nucleobases, that inhibit telomerase activity in
CC   mammalian cells by hybridising to the RNA component of mammalian
CC   telomerase. The PNAs are useful as probes to detect the RNA component
CC   of mammalian telomerase and as inhibitors of telomerase activity, or to
CC   detect and/or quantitate polynucleotide having the human telomerase
CC   RNA component (hTR) sequence, as well as in forensic identification of
CC   individuals, such as paternity testing or identification of criminal
CC   suspects or unknown descendants based on the hTR gene RFLP pattern. The
CC   PNA can be further used for treating or preventing cancer, inflammation,
CC   lymphoproliferative diseases, autoimmune disease, or neurodegenerative
CC   diseases. The PNAs in combination with other pharmaceuticals (such as
CC   antineoplastic or cytostatic agents) can be used for treating neoplasia,
CC   hyperplasia, human immunodeficiency virus (HIV) infections, acquired
CC   immunodeficiency syndrome (AIDS) and associated pathologies, and other
CC   diseases characterised by abnormal telomere metabolism or telomerase
CC   activity. The present sequence represents one of the PNA sequences
CC   of the invention.
XX
SQ   Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 23;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          7 CCCTAA 2


RESULT 13
AAS15474/c
ID   AAS15474 standard; DNA; 8 BP.
XX
AC   AAS15474;
XX
DT   14-FEB-2002  (first entry)
XX
DE   PNA 34 inhibiting human and mammalian telomerase activity.
XX
KW   Mammalian; peptide nucleic acid; probe; forensic; paternity testing;
KW   human telomerase RNA component; hTR gene RFLP pattern; cancer;
KW   inflammation; lymphoproliferative disease; autoimmune disease;
KW   neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS;
KW   human immunodeficiency virus; acquired immunodeficiency syndrome;
KW   telomere metabolism; mutant; cytostatic; anti-inflammatory;
KW   immunosuppressive; polyamide backbone; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..8
FT                   /*tag= a
FT                   /note= "This sequence is a peptide nucleic acid, i.e. it
FT                          contains a polyamide backbone instead of a
FT                          deoxyribose backbone"
FT   modified_base   1
FT                   /*tag= b
FT                   /note= "N= 1-50 peptide nucleic acid nucleobases,
FT                          selected from U, T, A, G, C or i"
FT   modified_base   8
FT                   /*tag= c
FT                   /note= "N= 1-50 peptide nucleic acid nucleobases,
FT                          selected from U, T, A, G, C or i"
XX
PN   US6294650-B1.
XX
PD   25-SEP-2001.
XX
PF   08-JUL-1999;   99US-0349532.
XX
PR   09-APR-1997;   97US-0838545.
PR   09-APR-1996;   96US-0630019.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Shay JW,  Wright WE,  Piatyszek MA,  Corey DR,  Norton JC;
XX
DR   WPI; 2001-638024/73.
XX
PT   New peptide nucleic acids that hybridises to the RNA component of
PT   mammalian telomerase, useful for treating or preventing cancer,
PT   inflammation, lymphoproliferative diseases, autoimmune disease, or
PT   neurodegenerative diseases  -
XX
PS   Disclosure; Column 59; 46pp; English.
XX
CC   The present invention relates to peptide nucleic acids (PNAs), comprising
CC   a sequence of 6-25 nucleobases, that inhibit telomerase activity in
CC   mammalian cells by hybridising to the RNA component of mammalian
CC   telomerase. The PNAs are useful as probes to detect the RNA component
CC   of mammalian telomerase and as inhibitors of telomerase activity, or to
CC   detect and/or quantitate polynucleotide having the human telomerase
CC   RNA component (hTR) sequence, as well as in forensic identification of
CC   individuals, such as paternity testing or identification of criminal
CC   suspects or unknown descendants based on the hTR gene RFLP pattern. The
CC   PNA can be further used for treating or preventing cancer, inflammation,
CC   lymphoproliferative diseases, autoimmune disease, or neurodegenerative
CC   diseases. The PNAs in combination with other pharmaceuticals (such as
CC   antineoplastic or cytostatic agents) can be used for treating neoplasia,
CC   hyperplasia, human immunodeficiency virus (HIV) infections, acquired
CC   immunodeficiency syndrome (AIDS) and associated pathologies, and other
CC   diseases characterised by abnormal telomere metabolism or telomerase
CC   activity. The present sequence represents one of the PNA sequences
CC   of the invention.
CC   Note: The present sequence is given in the SEQ ID listing but is not
CC   mentioned elsewhere in the patent.
XX
SQ   Sequence 8 BP; 1 A; 0 C; 3 G; 2 T; 2 other;

  Query Match             100.0%;  Score 6;  DB 23;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
CC   telomerase activity. Telomerase is a ribonucleoprotein enzyme that
CC   synthesizes one strand of the telomeric DNA, using as a template an 11
CC   nucleotide sequence contained within the RNA component of the enzyme. The
CC   invention relates to PNA molecules having a sequence of no more than 25
CC   bases, which include the sequence GTTAGG. The uncharged nature of the PNA
CC   backbone increases the melting temperature of associating strands,
CC   increases the rate of association with targeted nucleic acids, and
CC   affords greater resistance of degradation by proteases or nucleases. The
CC   therapeutic PNAs may be used for treating disease conditions such as
CC   cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
CC   immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
CC   syndrome) and associated pathologies, fungal infections, and other
CC   diseases characterized by abnormal telomere metabolism or telomerase
CC   activity, in combination with antineoplastic and other cytotoxic or
CC   cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
CC   used for molecular diagnostics, labelled PNAs are used as hybridization
CC   probes to detect or quantitate polynucleotides having a human telomerase
CC   RNA (hTR) sequence. PNA probes are also used for forensic identification
CC   of individuals, e.g. paternity testing, based on hTR gene restriction
CC   fragment length polymorphism (RFLP) pattern. PNAs are also useful as
CC   probes to detect the RNA component of a mammalian telomerase and as
CC   inhibitors of telomerase activity. The method of the present invention
CC   allows cancerous conditions to be detected with increased confidence and
CC   possibly at an earlier stage, before cells are detected as cancerous
CC   based on pathological characteristics. The diagnostic and prognostic
CC   methods of the present invention can be used to detect an immortal or
CC   neoplastic cell or tumour tissue or cancer of any origin, provided the
CC   cell expresses telomerase activity and its RNA component.
XX
SQ   Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 21;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          7 CCCTAA 2


RESULT 11
AAA37572
ID   AAA37572 standard; DNA; 8 BP.
XX
AC   AAA37572;
XX
DT   15-AUG-2000  (first entry)
XX
DE   PNA sequence #30 used to inhibit telomerase activity.
XX
KW   Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
KW   inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
KW   AIDS; HIV; fungal infection; forensic identification; detect; tumour;
KW   paternity testing; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..8
FT                   /*tag=  a
FT                   /note= "Peptide nucleic acid molecule, where
FT                          N-(2-aminoethyl)glycine units are linked to
FT                          nucleotide bases via glycine amino N through a
FT                          methylenecarbonyl linker"
XX
PN   US6046307-A.
XX
PD   04-APR-2000.
XX
PF   09-APR-1997;   97US-0838545.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Wright WE,  Piatyszek MA,  Shay JW,  Norton JC,  Corey DR;
XX
DR   WPI; 2000-292432/25.
XX
PT   New peptide nucleic acid (PNA) compounds that inhibit telomerase
PT   activity in mammalian cells is useful as probes to detect the RNA
PT   component of a mammalian telomerase  -
XX
PS   Example 2; Column 33; 45pp; English.
XX
CC   The present sequence represents a peptide nucleic acid molecule which
CC   hybridises to the mRNA component of mammalian telomerase, and inhibits
CC   telomerase activity. Telomerase is a ribonucleoprotein enzyme that
CC   synthesizes one strand of the telomeric DNA, using as a template an 11
CC   nucleotide sequence contained within the RNA component of the enzyme. The
CC   invention relates to PNA molecules having a sequence of no more than 25
CC   bases, which include the sequence GTTAGG. The uncharged nature of the PNA
CC   backbone increases the melting temperature of associating strands,
CC   increases the rate of association with targeted nucleic acids, and
CC   affords greater resistance of degradation by proteases or nucleases. The
CC   therapeutic PNAs may be used for treating disease conditions such as
CC   cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
CC   immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
CC   syndrome) and associated pathologies, fungal infections, and other
CC   diseases characterized by abnormal telomere metabolism or telomerase
CC   activity, in combination with antineoplastic and other cytotoxic or
CC   cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
CC   used for molecular diagnostics, labelled PNAs are used as hybridization
CC   probes to detect or quantitate polynucleotides having a human telomerase
CC   RNA (hTR) sequence. PNA probes are also used for forensic identification
CC   of individuals, e.g. paternity testing, based on hTR gene restriction
CC   fragment length polymorphism (RFLP) pattern. PNAs are also useful as
CC   probes to detect the RNA component of a mammalian telomerase and as
CC   inhibitors of telomerase activity. The method of the present invention
CC   allows cancerous conditions to be detected with increased confidence and
CC   possibly at an earlier stage, before cells are detected as cancerous
CC   based on pathological characteristics. The diagnostic and prognostic
CC   methods of the present invention can be used to detect an immortal or
CC   neoplastic cell or tumour tissue or cancer of any origin, provided the
CC   cell expresses telomerase activity and its RNA component.
XX
SQ   Sequence 8 BP; 3 A; 4 C; 0 G; 1 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 21;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          2 CCCTAA 7


RESULT 12
AAS15436/c
ID   AAS15436 standard; DNA; 8 BP.
XX
AC   AAS15436;
XX
DT   14-FEB-2002  (first entry)
XX
DE   PNA 28 inhibiting human and mammalian telomerase activity.
XX
KW   Mammalian; peptide nucleic acid; probe; forensic; paternity testing;
KW   human telomerase RNA component; hTR gene RFLP pattern; cancer;
KW   inflammation; lymphoproliferative disease; autoimmune disease;
KW   neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS;
KW   human immunodeficiency virus; acquired immunodeficiency syndrome;
KW   telomere metabolism; mutant; cytostatic; anti-inflammatory;
KW   immunosuppressive; polyamide backbone; ss.
XX
OS   Homo sapiens.
```

```
XX
PT   Oligomer hybridisable to HIV sequence and contg. peptide nucleic
PT   acid sub:unit - binds in complementary manner to DNA and RNA, and
PT   useful for modulating HIV viral activity, e.g. in treating AIDS
XX
PS   Claim 2; Page 176; 186pp; English.
XX
CC   New peptide nucleic acid (PNA) oligomers are provided which (a) consist
CC   of naturally occurring nucleobases covalently bound to a polyamide
CC   backbone and (b) hybridise to the translation initiation AUG region,
CC   5' untranslated region (5' UTR), 3' untranslated region (3' UTR),
CC   splice junctions or coding sequence of a human immunodeficiency virus
CC   gene chosen from env, gag, pol, rev and tat.
CC   The PNAs can be used to target RNA and single stranded DNA (ssDNA) to
CC   produce antisense-type gene regulation moieties. They have utility
CC   as gene-targetted drugs for modulating HIV processes. Hence they
CC   can be used to treat AIDS and other viral infections. They are also
CC   useful in diagnostic applications and as research tools.
CC   PNA oligomers have high affinity for complementary single stranded DNA.
CC   They are also able to form triple helices in which a first PNA strand
CC   binds with RNA or ssDNA and a second PNA strand binds with the resulting
CC   double helix or with the first PNA strand. The PNAs possess no
CC   significant charge and are water soluble, which facilitates cellular
CC   uptake. Further, since they contain amides of non-biological amino acids,
CC   they are biostable and resistant to enzymatic degradation by proteases.
CC   The present sequence is a specifically claimed PNA sequence
CC   (represented by the sequence of nucleobases) targetting HIV genes.
XX
SQ   Sequence 8 BP; 1 A; 0 C; 3 G; 4 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 16;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 9
AAT89239/c
ID   AAT89239 standard; DNA; 8 BP.
XX
AC   AAT89239;
XX
DT   12-MAY-1998  (first entry)
XX
DE   Peptide nucleic acid 14, targeted to mammalian telomerase.
XX
KW   Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
KW   inhibitor; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1..8
FT                    /*tag=  a
FT                    /note= "Sugar-phosphate backbone has been replaced by
FT                           a peptide backbone"
XX
PN   WO9738013-A1.
XX
PD   16-OCT-1997.
XX
PF   09-APR-1997;   97WO-US05931.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (GERO-) GERON CORP.
XX
PI   Corey D,  Norton JC,  Piatyszek MA,  Shay JW,  Wright WE;
XX
DR   WPI; 1997-512647/47.
XX
PT   New peptide nucleic acids hybridising to mammalian telomerase RNA -
PT   used to inhibit telomerase, for treating tumours and other
PT   proliferative diseases, also for diagnosis
XX
PS   Claim 9; Page 59; 76pp; English.
XX
CC   This sequence is a novel peptide nucleic acid (PNA), which acts as
CC   an inhibitor of mammalian, preferably human, telomerase.  The PNAs
CC   hybridise specifically to an RNA component of mammalian telomerase,
CC   and include the sequence GGG for specific hybridisation to the template
CC   region of this component.  PNAs can be used as probes to detect the
CC   RNA component of mammalian telomerase and as inhibitors of telomerase
CC   activity, especially in the treatment of cancer.
XX
SQ   Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 18;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          7 CCCTAA 2


RESULT 10
AAA37558/c
ID   AAA37558 standard; DNA; 8 BP.
XX
AC   AAA37558;
XX
DT   15-AUG-2000  (first entry)
XX
DE   PNA sequence #15 used to inhibit telomerase activity.
XX
KW   Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
KW   inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
KW   AIDS; HIV; fungal infection; forensic identification; detect; tumour;
KW   paternity testing; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..8
FT                   /*tag=  a
FT                   /note= "Peptide nucleic acid molecule, where
FT                          N-(2-aminoethyl)glycine units are linked to
FT                          nucleotide bases via glycine amino N through a
FT                          methylenecarbonyl linker"
XX
PN   US6046307-A.
XX
PD   04-APR-2000.
XX
PF   09-APR-1997;   97US-0838545.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Wright WE,  Piatyszek MA,  Shay JW,  Norton JC,  Corey DR;
XX
DR   WPI; 2000-292432/25.
XX
PT   New peptide nucleic acid (PNA) compounds that inhibit telomerase
PT   activity in mammalian cells is useful as probes to detect the RNA
PT   component of a mammalian telomerase  -
XX
PS   Claim 6; Column 71; 45pp; English.
XX
CC   The present sequence represents a peptide nucleic acid molecule which
CC   hybridises to the mRNA component of mammalian telomerase, and inhibits
```

```
Db          6 CCCTAA 1


RESULT 6
AAN91439
ID   AAN91439 standard; DNA; 7 BP.
XX
AC   AAN91439;
XX
DT   22-FEB-1990  (first entry)
XX
DE   Telomere of Arabidopsis thaliana.
XX
KW   Telomere; Arabidopsis thaliana; vector; artificial chromosomes;
KW   tandem repeat.
XX
OS   Arabidopsis thaliana.
XX
PN   WO8909219-A.
XX
PD   05-OCT-1989.
XX
PF   27-FEB-1989;   89WO-US00795.
XX
PR   24-MAR-1988;   88US-0172467.
XX
PA   (GEHO-) THE GENERAL HOSPITAL CORP.
XX
PI   Richards E,  Ausubel FM;
XX
DR   WPI; 1989-309497/42.
XX
PT   New recombinant DNA contg. eukaryotic telomere esp. from higher plant
PT   - useful as vector for specific genes and maintained in nucleus as
PT   independent replicating molecule.
XX
PS   Claim 28; page 50; 65pp; English.
XX
CC   Tandem repeats (1-1000) of the telomere are used in a vector for
CC   expressing specific genes in plants. They provide 'artificial
CC   chromosomes' which are maintained in the nucleus, so are not subjected to
CC   variable expression due to integration-position effects. They allow the
CC   integration of very foreign DNA without host range limitations.
CC   The telomere opt. contains variant repeats of CTCTAAA. The telomere is
CC   pref. the pAtT4 plasmid (ATCC 67577).
XX
SQ   Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 10;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          1 CCCTAA 6


RESULT 7
AAN91442
ID   AAN91442 standard; DNA; 7 BP.
XX
AC   AAN91442;
XX
DT   22-FEB-1990  (first entry)
XX
DE   Variant of Arabidopsis thaliana telomere.
XX
KW   Variant telomere; Arabidopsis thaliana; vector; artificial chromosomes;
KW   tandem repeat.
XX
OS   Arabidopsis thaliana.
XX
PN   WO8909219-A.
XX
PD   05-OCT-1989.
XX
PF   27-FEB-1989;   89WO-US00795.
XX
PR   24-MAR-1988;   88US-0172467.
XX
PA   (GEHO-) THE GENERAL HOSPITAL CORP.
XX
PI   Richards E,  Ausubel FM;
XX
DR   WPI; 1989-309497/42.
XX
PT   New recombinant DNA contg. eukaryotic telomere esp. from higher plant
PT   - useful as vector for specific genes and maintained in nucleus as
PT   independent replicating molecule.
XX
PS   Claim 35; page 50; 65pp; English.
XX
CC   The DNA is a variant of the telomere of the pAtT4 plasmid (ATCC 67577).
XX
SQ   Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 10;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          1 CCCTAA 6


RESULT 8
AAQ97993/c
ID   AAQ97993 standard; DNA; 8 BP.
XX
AC   AAQ97993;
XX
DT   19-OCT-1995  (first entry)
XX
DE   Peptide nucleic acid oligomer targetting HIV gene.
XX
KW   Peptide nucleic acid; PNA; HIV; human immunodeficiency virus;
KW   AIDS; antiviral; antisense; triple helix; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..8
FT                   /*tag=  a
FT                   /note= "at least one (and preferably all) of
FT                          the backbone subunits are composed of N-acetyl
FT                          N-(2-aminoethyl)glycine peptide residues, the
FT                          nucleobase being attached covalently to the
FT                          acetyl group and the peptide linkage being
FT                          formed by condensation of the glycine
FT                          carboxy group of one residue with the amino
FT                          group of the 2-aminoethyl moiety in the next
FT                          residue"
XX
PN   WO9504068-A.
XX
PD   09-FEB-1995.
XX
PF   28-JUL-1994;   94WO-US08517.
XX
PR   29-JUL-1993;   93US-0099718.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ecker DJ;
XX
DR   WPI; 1995-082179/11.
```

```
XX
SQ   Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;

  Query Match            100.0%;  Score 6;  DB 23;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 4
AAS14916
ID   AAS14916 standard; DNA; 6 BP.
XX
AC   AAS14916;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Melanogenesis associated oligonucleotide #12.
XX
KW   Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW   anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW   immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW   tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW   carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW   conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS   Synthetic.
XX
PN   WO200174342-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US10162.
XX
PR   31-MAR-2000; 2000US-0540843.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Gilchrest BA,  Yaar M,  Eller M;
XX
DR   WPI; 2001-626338/72.
XX
PT   Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT   carcinoma, using specific oligonucleotides that mimic the effects of
PT   ultra-violet light -
XX
PS   Claim 1; Page 37; 74pp; English.
XX
CC   The invention describes inhibition of mammalian epithelial cell
CC   proliferation by treating cells with at least one oligonucleotide, or
CC   its fragment. The compounds, which have cytostatic, anti-allergic,
CC   anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC   immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC   DNA repair processes (or a protective response to later exposure to
CC   radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC   or a tumour necrosis factor inhibitor. Probably they mimic products of
CC   DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC   pathway, resulting in transient arrest of cell growth, allowing more time
CC   for DNA repair to occur before cell division takes place. The method is
CC   especially used to treat carcinoma but may also be used to: treat other
CC   hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC   reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC   allergically mediated inflammation (atopic or contact dermatitis,
CC   allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC   cells caused by radiation or chemicals; increase melanin production
CC   (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC   promote apoptosis in epithelial cells that contain damaged DNA. Also
CC   oligonucleotides that contain non-hydrolyzable backbones are used to
CC   inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC   sequence is melanogenesis associated oligonucleotide #12, the reverse
CC   complementary sequence of AAS149015, a truncated version of the sequence
CC   representing the telomere over-hang sequence (AAS14909), described in the
CC   method of the invention.
XX
SQ   Sequence 6 BP; 2 A; 3 C; 0 G; 1 T; 0 other;

  Query Match            100.0%;  Score 6;  DB 23;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          1 CCCTAA 6


RESULT 5
ABN73654/c
ID   ABN73654 standard; cDNA; 6 BP.
XX
AC   ABN73654;
XX
DT   03-JUL-2002  (first entry)
XX
DE   Bovine embryonic germ (EG) cell cDNA EST 990913a CONTIG 1.
XX
KW   Bovine; Bos taurus; EST; expressed sequence tag; totipotence;
KW   development; gene; ss.
XX
OS   Bos taurus.
XX
PN   WO200194550-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US18576.
XX
PR   07-JUN-2000; 2000US-209874P.
PR   06-JUN-2001; 2001US-0876143.
XX
PA   (INFI-) INFIGEN INC.
XX
PI   Eilertsen KJ,  Pfister-Genskow M,  Childs L;
XX
DR   WPI; 2002-351289/38.
XX
PT   An expressed sequence tag (EST), the expression of which, or its
PT   complementary sequence, in a cell identifies the cell as a
PT   developmentally competent or incompetent cell -
XX
PS   Example 16; Page 210; 584pp; English.
XX
CC   The present invention describes an expressed sequence tag (EST), where
CC   the EST is an isolated, enriched, or purified nucleic acid sequence
CC   representing all or part of a gene, the expression of which, or its
CC   complementary sequence, in a cell identifies the cell as a
CC   developmentally competent or incompetent cell. Molecules which induce
CC   developmental competence in a cell line are useful for inducing
CC   totipotence in one or more cells. Molecules which induce developmental
CC   incompetence in a cell line are useful for preventing a full term
CC   pregnancy in an animal and inhibiting totipotence. The molecules are
CC   also useful for treating a disease in an animal by inducing development
CC   of one or more cells of the animal into a specific cell type. The
CC   present sequence represents a bovine EST which is given in the
CC   exemplification of the present invention.
XX
SQ   Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;

  Query Match            100.0%;  Score 6;  DB 24;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
```

PT capacity and therefore delay cellular senescence, useful in cell
PT therapy and transplantation
XX
PS Claim 12; Page 29; 38pp; English.
XX
CC Oligonucleotides AAT05734-7 are examples of telomerase substrates used
CC to increase the proliferative capacity of normal cells that express
CC telomerase activity. The oligonucleotides allow an increase in
CC length of telomeres in normal cells and in hybrids of normal and
CC immortalised cells. The increase in telomere length extends the
CC capacity of cells to replicate, esp. those treated ex vivo and used
CC for transplantation techniques e.g. cell therapy, for the treatment
CC of AIDS, anaemia, leukaemia or lymphoma.
XX
SQ Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;

Query Match 100.0%; Score 6; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.6e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTAA 6
||||||
Db 6 CCCTAA 1

RESULT 2
AAX80998/c
ID AAX80998 standard; DNA; 6 BP.
XX
AC AAX80998;
XX
DT 13-SEP-1999 (first entry)
XX
DE Telomeric repeat sequence.
XX
KW Telomerase reverse transcriptase; TERT; mouse; telomere length assay;
KW immunogen; enzyme; telomerase-mediated DNA replication; human; ss.
XX
OS Homo sapiens.
XX
PN WO9927113-A1.
XX
PD 03-JUN-1999.
XX
PF 25-NOV-1998; 98WO-US25211.
XX
PR 16-MAR-1998; 98US-0042460.
PR 26-NOV-1997; 97US-0979742.
XX
PA (GERO-) GERON CORP.
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
XX
PI Allsopp R, Depinho R, Greenberg R, Morin GB;
XX
DR WPI; 1999-347722/29.
XX
PT Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and
PT nucleic acids
XX
PS Disclosure; Page 62; 135pp; English.
XX
CC The invention relates to a mouse telomerase reverse transcriptase (mTERT)
CC enzyme. Compositions containing mTERT can be used in telomere length
CC assays. Isolated mTERT is useful as an immunogen for the production of
CC monoclonal or polyclonal antibodies. The method is useful for assessing
CC the degree of purification and identification of new mTERT species, such
CC as an mTERT allele, homolog or isoform, or to screen for modulators
CC (antagonists and agonists) of telomerase-mediated DNA replication.
CC Antagonists and agonists of mTERT can be used to modify the activity of
CC other telomerase enzymes such as human TERT (hTERT).
XX
SQ Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;

Query Match 100.0%; Score 6; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.6e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTAA 6
||||||
Db 6 CCCTAA 1

RESULT 3
AAS14915/c
ID AAS14915 standard; DNA; 6 BP.
XX
AC AAS14915;
XX
DT 14-FEB-2002 (first entry)
XX
DE Melanogenesis assocaited oligonucleotide #11.
XX
KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS Synthetic.
XX
PN WO200174342-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10162.
XX
PR 31-MAR-2000; 2000US-0540843.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrest BA, Yaar M, Eller M;
XX
DR WPI; 2001-626338/72.
XX
PT Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT carcinoma, using specific oligonucleotides that mimic the effects of
PT ultra-violet light -
XX
PS Claim 1; Page 37; 74pp; English.
XX
CC The invention describes inhibition of mammalian epithelial cell
CC proliferation by treating cells with at least one oligonucleotide, or
CC its fragment. The compounds, which have cytostatic, anti-allergic,
CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC DNA repair processes (or a protective response to later exposure to
CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC or a tumour necrosis factor inhibitor. Probably they mimic products of
CC DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC pathway, resulting in transient arrest of cell growth, allowing more time
CC for DNA repair to occur before cell division takes place. The method is
CC especially used to treat carcinoma but may also be used to: treat other
CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC allergically mediated inflammation (atopic or contact dermatitis,
CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC cells caused by radiation or chemicals; increase melanin production
CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC promote apoptosis in epithelial cells that contain damaged DNA. Also
CC oligonucleotides that contain non-hydrolyzable backbones are used to
CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC sequence is melanogenesis associated oligonucleotide #11, a truncated
CC version of the sequence representing the telomere over-hang sequence
CC (AAS14909) and one of the oligonucleotides used to inhibit mammalian
CC epithelial cell proliferation, described in the method of the invention.

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 06:40:37 ; Search time 132.857 Seconds
(without alignments)
101.703 Million cell updates/sec

Title: US-09-540-843-12
Perfect score: 6
Sequence: 1 ccctaa 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2063506

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
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14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
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19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	6	100.0	6	16	AAT05734	Telomerase oligonu
c	2	6	100.0	6	20	AAX80998	Telomeric repeat s
c	3	6	100.0	6	23	AAS14915	Melanogenesis asso
	4	6	100.0	6	23	AAS14916	Melanogenesis asso
c	5	6	100.0	6	24	ABN73654	Bovine embryonic g
	6	6	100.0	7	10	AAN91439	Telomere of Arabid
	7	6	100.0	7	10	AAN91442	Variant of Arabido
c	8	6	100.0	8	16	AAQ97993	Peptide nucleic ac
c	9	6	100.0	8	18	AAT89239	Peptide nucleic ac
c	10	6	100.0	8	21	AAA37558	PNA sequence #15 u
	11	6	100.0	8	21	AAA37572	PNA sequence #30 u
c	12	6	100.0	8	23	AAS15436	PNA 28 inhibiting
c	13	6	100.0	8	23	AAS15474	PNA 34 inhibiting
c	14	6	100.0	9	16	AAT05735	Telomerase oligonu
c	15	6	100.0	9	18	AAT89240	Peptide nucleic ac
c	16	6	100.0	9	18	AAT93240	Telomerase substra
c	17	6	100.0	9	20	AAX21987	Telomere motif mim
c	18	6	100.0	9	21	AAA37559	PNA sequence #16 u
c	19	6	100.0	9	21	AAZ56813	Primer for human t
c	20	6	100.0	9	22	AAL20082	Human breast cance
c	21	6	100.0	9	23	AAS15437	PNA 29 inhibiting
	22	6	100.0	9	24	ABK87319	Drosophila Bicoid
c	23	6	100.0	10	18	AAV07770	N3 to P5 oligonucl
c	24	6	100.0	10	18	AAV07771	N3 to P5 oligonucl
c	25	6	100.0	10	18	AAT89241	Peptide nucleic ac
	26	6	100.0	10	18	AAT89249	DNA oligonucleotid
c	27	6	100.0	10	18	AAT89231	Peptide nucleic ac
	28	6	100.0	10	19	AAV41382	Antisense oligonuc
	29	6	100.0	10	20	AAZ28358	Lung cancer indica
c	30	6	100.0	10	20	AAX22183	Random amplified p
c	31	6	100.0	10	20	AAX21986	Telomere motif mim
c	32	6	100.0	10	20	AAX21995	Telomere motif mim
c	33	6	100.0	10	21	AAA56520	Human macrophage g
c	34	6	100.0	10	21	AAA37550	PNA sequence #7 us
	35	6	100.0	10	21	AAA37554	Template region of
c	36	6	100.0	10	21	AAA37560	PNA sequence #17 u
c	37	6	100.0	10	21	AAA37563	PNA sequence #21 u
	38	6	100.0	10	21	AAA37571	PNA sequence #29 u
c	39	6	100.0	10	21	AAZ77628	Human dendritic ce
c	40	6	100.0	10	21	AAZ77930	Human dendritic ce
c	41	6	100.0	10	21	AAZ78185	Human dendritic ce
c	42	6	100.0	10	21	AAZ79266	Human dendritic ce
c	43	6	100.0	10	21	AAZ80922	Metastatic breast
	44	6	100.0	10	21	AAZ81372	Metastatic breast
	45	6	100.0	10	21	AAZ81511	Metastatic breast

ALIGNMENTS

RESULT 1
AAT05734/c
ID AAT05734 standard; DNA; 6 BP.
XX
AC AAT05734;
XX
DT 01-FEB-1996 (first entry)
XX
DE Telomerase oligonucleotide substrate #1.
XX
KW Telomerase; proliferation; telomere; hybrid; immortalised cell; anaemia;
KW transplantation; cell therapy; treatment; AIDS; leukaemia; lymphoma; ss.
XX
OS Synthetic.
XX
PN WO9513383-A1.
XX
PD 18-MAY-1995.
XX
PF 10-NOV-1994; 94WO-US13130.
XX
PR 12-NOV-1993; 93US-0153051.
PR 12-NOV-1993; 93US-0151477.
XX
PA (GERO-) GERON CORP.
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Shay J, West MD, Wright WE;
XX
DR WPI; 1995-224051/29.
XX
PT Increasing telomere length in cells - to increase proliferative

```
REFERENCE   1  (bases 1 to 21)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821108.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 10
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 21 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM5  row: P  column: 5
            High quality sequence stop: 10.
FEATURES              Location/Qualifiers
     source           1. .21
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2821108"
                      /clone_lib="NIH_MGC_7"
                      /tissue_type="small cell carcinoma"
                      /cell_line="MGC3"
                      /lab_host="DH10B (phage-resistant)"
                      /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                      EcoRI; cDNA made by oligo-dT priming.  Directionally
                      cloned into EcoRI/XhoI sites using the following 5'
                      adaptor: GGCACGAG(G).  Size-selected >500bp for average
                      insert size 1.8kb.  Library constructed by Ling Hong in
                      the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      4 a      6 c      0 g      11 t
ORIGIN

  Query Match           100.0%;  Score 6;  DB 10;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 4.5e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db         15 CCCTAA 20


RESULT 15
AZ331625
LOCUS       AZ331625                 21 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0059M07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0059M07 R, DNA sequence.
ACCESSION   AZ331625
VERSION     AZ331625.1  GI:10394498
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0059  row: M  column: 07
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES              Location/Qualifiers
     source           1. .21
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0059M07"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT      8 a      7 c      0 g      6 t
ORIGIN

  Query Match           100.0%;  Score 6;  DB 17;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 4.5e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db         11 CCCTAA 16


Search completed: July  6, 2003, 09:39:51
Job time : 894.643 secs
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                     /organism="Trypanosoma brucei"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="158a03"
BASE COUNT         6 a      11 c       0 g       3 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 17;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          2 CCCTAA 7


RESULT 12
TA199G02Q
LOCUS       TA199G02Q                 20 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 199g02, reverse sequence,
            genomic survey sequence.
ACCESSION   AL476798
VERSION     AL476798.1  GI:11843362
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Trypanosoma brucei"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="199g02"
BASE COUNT         5 a      4 c       3 g       8 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 17;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db         15 CCCTAA 20


RESULT 13
AW248826
LOCUS       AW248826                  21 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821056.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821056 3',
            mRNA sequence.
ACCESSION   AW248826
VERSION     AW248826.1  GI:6591819
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821056.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 21
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 21 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM5  row: N  column: 1
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821056"
                     /clone_lib="NIH_MGC_7"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT         4 a      3 c       3 g      11 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 10;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db         15 CCCTAA 20


RESULT 14
AW248836
LOCUS       AW248836                  21 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821108.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821108 3',
            mRNA sequence.
ACCESSION   AW248836
VERSION     AW248836.1  GI:6591829
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0071D09"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 2 c 10 g 6 t
ORIGIN

Query Match 100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTAA 6
||||||
Db 11 CCCTAA 6

RESULT 10
AZ960008
LOCUS AZ960008 20 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0227G21R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0227G21 R, DNA sequence.
ACCESSION AZ960008
VERSION AZ960008.1 GI:13831235
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0227 row: G column: 21
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0227G21"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 8 a 5 c 2 g 5 t
ORIGIN

Query Match 100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTAA 6
||||||
Db 13 CCCTAA 18

RESULT 11
TA158A03P
LOCUS TA158A03P 20 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 158a03, forward sequence, genomic survey sequence.
ACCESSION AL472050
VERSION AL472050.1 GI:11837404
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 20)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES Location/Qualifiers
source 1. .20

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0467O10"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 2 c 7 g 6 t
ORIGIN

Query Match 100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTAA 6
||||||
Db 18 CCCTAA 13

RESULT 8
AZ662909/c
LOCUS AZ662909 20 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0542G17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0542G17 F, DNA sequence.
ACCESSION AZ662909
VERSION AZ662909.1 GI:11800055
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0542 row: G column: 17
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0542G17"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 2 c 11 g 5 t
ORIGIN

Query Match 100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTAA 6
||||||
Db 12 CCCTAA 7

RESULT 9
AZ808291/c
LOCUS AZ808291 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0071D09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0071D09 R, DNA sequence.
ACCESSION AZ808291
VERSION AZ808291.1 GI:12973320
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0071 row: D column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0102N07"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 8 a 6 c 2 g 3 t
ORIGIN

Query Match 100.0%; Score 6; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTAA 6
||||||
Db 12 CCCTAA 17

RESULT 6
AZ345513
LOCUS AZ345513 20 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0080J04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080J04 F, DNA sequence.
ACCESSION AZ345513
VERSION AZ345513.1 GI:10424750
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: J column: 04
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080J04"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 13 c 0 g 4 t
ORIGIN

Query Match 100.0%; Score 6; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTAA 6
||||||
Db 11 CCCTAA 16

RESULT 7
AZ627174/c
LOCUS AZ627174 20 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0467O10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0467O10 R, DNA sequence.
ACCESSION AZ627174
VERSION AZ627174.1 GI:11749364
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0467 row: O column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0200F10"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 5 c 2 g 5 t
ORIGIN

Query Match 100.0%; Score 6; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTAA 6
||||||
Db 3 CCCTAA 8

RESULT 4
AZ614760/c
LOCUS AZ614760 19 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0443A17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0443A17 R, DNA sequence.
ACCESSION AZ614760
VERSION AZ614760.1 GI:11736950
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0443 row: A column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0443A17"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 0 c 10 g 6 t
ORIGIN

Query Match 100.0%; Score 6; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTAA 6
||||||
Db 15 CCCTAA 10

RESULT 5
AZ826736
LOCUS AZ826736 19 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0102N07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0102N07 R, DNA sequence.
ACCESSION AZ826736
VERSION AZ826736.1 GI:12996644
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0102 row: N column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19

```
            http://www.genome.washington.edu Low Quality Sequence: 15
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 16 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM1  row: K  column: 7
            High quality sequence stop: 15.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2819454"
                      /clone_lib="NIH_MGC_7"
                      /tissue_type="small cell carcinoma"
                      /cell_line="MGC3"
                      /lab_host="DH10B (phage-resistant)"
                      /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                      EcoRI; cDNA made by oligo-dT priming.  Directionally
                      cloned into EcoRI/XhoI sites using the following 5'
                      adaptor: GGCACGAG(G).  Size-selected >500bp for average
                      insert size 1.8kb.  Library constructed by Ling Hong in
                      the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT        3 a      0 c      3 g     10 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 10;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db         14 CCCTAA 9


RESULT 2
AZ392246/c
LOCUS       AZ392246                 19 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0154G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0154G12 R, DNA sequence.
ACCESSION   AZ392246
VERSION     AZ392246.1  GI:10507234
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0154  row: G  column: 12
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0154G12"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT        3 a      5 c      5 g      6 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 17;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db         19 CCCTAA 14


RESULT 3
AZ422271
LOCUS       AZ422271                 19 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0200F10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0200F10 R, DNA sequence.
ACCESSION   AZ422271
VERSION     AZ422271.1  GI:10546284
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0200  row: F  column: 10
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 07:33:45 ; Search time 894.643 Seconds
(without alignments)
108.616 Million cell updates/sec

Title: US-09-540-843-12
Perfect score: 6
Sequence: 1 ccctaa 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 60474

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	6	100.0	16	10	AW248958	AW248958 2819454.3
c	2	6	100.0	19	17	AZ392246	AZ392246 1M0154G12
	3	6	100.0	19	17	AZ422271	AZ422271 1M0200F10
c	4	6	100.0	19	17	AZ614760	AZ614760 1M0443A17
	5	6	100.0	19	17	AZ826736	AZ826736 2M0102N07
	6	6	100.0	20	17	AZ345513	AZ345513 1M0080J04
c	7	6	100.0	20	17	AZ627174	AZ627174 1M0467O10
c	8	6	100.0	20	17	AZ662909	AZ662909 1M0542G17
c	9	6	100.0	20	17	AZ808291	AZ808291 2M0071D09
	10	6	100.0	20	17	AZ960008	AZ960008 2M0227G21
	11	6	100.0	20	17	TA158A03P	AL472050 T. brucei
	12	6	100.0	20	17	TA199G02Q	AL476798 T. brucei
	13	6	100.0	21	10	AW248826	AW248826 2821056.3
	14	6	100.0	21	10	AW248836	AW248836 2821108.3
	15	6	100.0	21	17	AZ331625	AZ331625 1M0059M07
	16	6	100.0	21	17	AZ399400	AZ399400 1M0165C13
	17	6	100.0	21	17	AZ445481	AZ445481 1M0241P15
	18	6	100.0	21	17	AZ626594	AZ626594 1M0466J20
	19	6	100.0	21	17	AZ760907	AZ760907 1M0554P21
c	20	6	100.0	21	17	AZ766315	AZ766315 1M0563K14
	21	6	100.0	21	17	AZ828389	AZ828389 2M0105P16
	22	6	100.0	21	17	AZ833919	AZ833919 2M0116N18
	23	6	100.0	21	17	AZ877328	AZ877328 2M0192C18
	24	6	100.0	22	9	AA954126	AA954126 oq66a07.s
c	25	6	100.0	22	9	AA527213	AA527213 ni27b11.s
	26	6	100.0	22	14	D18745	D18745 MUSGS01807
	27	6	100.0	22	17	AZ324747	AZ324747 1M0046O13
	28	6	100.0	22	17	AZ464647	AZ464647 1M0274D09
c	29	6	100.0	22	17	AZ483833	AZ483833 1M0310H03
c	30	6	100.0	22	17	AZ500414	AZ500414 1M0338G17
	31	6	100.0	22	17	AZ598320	AZ598320 1M0413N04
	32	6	100.0	22	17	AZ629501	AZ629501 1M0482G06
c	33	6	100.0	22	17	AZ666649	AZ666649 1M0548M19
c	34	6	100.0	22	17	AZ836104	AZ836104 2M0130C17
	35	6	100.0	22	17	AZ855118	AZ855118 2M0159H05
	36	6	100.0	23	9	AU258772	AU258772 AU258772
	37	6	100.0	23	17	AZ423815	AZ423815 1M0203O23
c	38	6	100.0	23	17	AZ465280	AZ465280 1M0275A10
c	39	6	100.0	23	17	AZ623979	AZ623979 1M0462E14
c	40	6	100.0	23	17	AZ817008	AZ817008 2M0086E02
	41	6	100.0	23	17	AZ979817	AZ979817 2M0256F09
c	42	6	100.0	23	17	BH857265	BH857265 SALK_0765
	43	6	100.0	24	17	AZ309633	AZ309633 1M0016B22
c	44	6	100.0	24	17	AZ785628	AZ785628 2M0029M09
c	45	6	100.0	24	17	AZ806300	AZ806300 2M0068F13

ALIGNMENTS

RESULT 1
AW248958/c
LOCUS AW248958 16 bp mRNA linear EST 07-JAN-2000
DEFINITION 2819454.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819454 3', mRNA sequence.
ACCESSION AW248958
VERSION AW248958.1 GI:6591951
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 16)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2819454.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center:

Search completed: July 6, 2003, 12:17:04
Job time : 65.5714 secs

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  Best Local Similarity   100.0%;  Pred. No. 1.7e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          1 CCCTAA 6


RESULT 14
US-10-044-692-294/c
; Sequence 294, Application US/10044692
; Publication No. US20030096344A1
;   GENERAL INFORMATION:
;        APPLICANT: Cech, Thomas R.
;                   Lingner, Joachim
;                   Nakamura, Toru
;                   Chapman, Karen B.
;                   Morin, Gregg B.
;                   Harley, Calvin
;                   Andrews, William H.
;        TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:  DIAGNOSTIC AND
;                            THERAPEUTIC METHODS
;        NUMBER OF SEQUENCES: 335
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, 8th Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/044,692
;             FILING DATE: 11-Jan-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/912,951
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: US 08/854,050
;             FILING DATE: 09-MAY-1997
;             APPLICATION NUMBER: US 08/851,843
;             FILING DATE: 06-MAY-1997
;             APPLICATION NUMBER: US 08/846,017
;             FILING DATE: 25-APR-1997
;             APPLICATION NUMBER: US 08/844,419
;             FILING DATE: 18-APR-1997
;             APPLICATION NUMBER: US 08/724,643
;             FILING DATE: 01-OCT-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Apple,  Randolph T.
;             REGISTRATION NUMBER: 36,429
;             REFERENCE/DOCKET NUMBER: 015389-002600US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 294:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 10 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 294:
US-10-044-692-294

  Query Match           100.0%;  Score 6;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 15
US-10-044-539-294/c
; Sequence 294, Application US/10044539
; Publication No. US20030100093A1
;   GENERAL INFORMATION:
;        APPLICANT: Cech, Thomas R.
;                   Lingner, Joachim
;                   Nakamura, Toru
;                   Chapman, Karen B.
;                   Morin, Gregg B.
;                   Harley, Calvin
;                   Andrews, William H.
;        TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:  DIAGNOSTIC AND
;                            THERAPEUTIC METHODS
;        NUMBER OF SEQUENCES: 335
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, 8th Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/044,539
;             FILING DATE: 11-Jan-2002
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/912,951
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: US 08/854,050
;             FILING DATE: 09-MAY-1997
;             APPLICATION NUMBER: US 08/851,843
;             FILING DATE: 06-MAY-1997
;             APPLICATION NUMBER: US 08/846,017
;             FILING DATE: 25-APR-1997
;             APPLICATION NUMBER: US 08/844,419
;             FILING DATE: 18-APR-1997
;             APPLICATION NUMBER: US 08/724,643
;             FILING DATE: 01-OCT-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Apple,  Randolph T.
;             REGISTRATION NUMBER: 36,429
;             REFERENCE/DOCKET NUMBER: 015389-002600US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 294:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 10 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 294:
US-10-044-539-294

  Query Match           100.0%;  Score 6;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1
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Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 10
US-09-730-893-6/c
; Sequence 6, Application US/09730893
; Patent No. US20020107258A1
; GENERAL INFORMATION:
;  APPLICANT: KERWIN, SEAN M.
;  APPLICANT:  FEDOROFF, OLEG Y.
;  APPLICANT:  SALAZAR, MIGUEL
;  APPLICANT:  HURLEY, LAURENCE H.
;  TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
;  TITLE OF INVENTION:  G-QUADRUPLEX-INTERACTION COMPOUND
;  FILE REFERENCE: UTSB:679USC1
;  CURRENT APPLICATION NUMBER: US/09/730,893
;  CURRENT FILING DATE:  2000-12-05
;  PRIOR APPLICATION NUMBER: 09/244,675
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: 60/073,629
;  PRIOR FILING DATE: 1998-04-02
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-09-730-893-6

  Query Match            100.0%;  Score 6;  DB 10;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 11
US-09-940-173A-4/c
; Sequence 4, Application US/09940173A
; Publication No. US20030040525A1
; GENERAL INFORMATION:
;  APPLICANT: KERWIN, SEAN M.
;  APPLICANT:  FEDOROFF, OLEG Y.
;  APPLICANT:  SALAZAR, MIGUEL
;  APPLICANT:  HURLEY, LAURENCE H.
;  TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
;  TITLE OF INVENTION:  G-QUADRUPLEX-INTERACTION COMPOUND
;  FILE REFERENCE: UTSB:679USD2
;  CURRENT APPLICATION NUMBER: US/09/940,173A
;  CURRENT FILING DATE:  2002-06-24
;  PRIOR APPLICATION NUMBER: 09/730,893
;  PRIOR FILING DATE: 2000-12-05
;  PRIOR APPLICATION NUMBER: 09/244,675
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: 60/073,629
;  PRIOR FILING DATE: 1998-04-02
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-09-940-173A-4

  Query Match            100.0%;  Score 6;  DB 9;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 12
US-09-730-893-4/c
; Sequence 4, Application US/09730893
; Patent No. US20020107258A1
; GENERAL INFORMATION:
;  APPLICANT: KERWIN, SEAN M.
;  APPLICANT:  FEDOROFF, OLEG Y.
;  APPLICANT:  SALAZAR, MIGUEL
;  APPLICANT:  HURLEY, LAURENCE H.
;  TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
;  TITLE OF INVENTION:  G-QUADRUPLEX-INTERACTION COMPOUND
;  FILE REFERENCE: UTSB:679USC1
;  CURRENT APPLICATION NUMBER: US/09/730,893
;  CURRENT FILING DATE:  2000-12-05
;  PRIOR APPLICATION NUMBER: 09/244,675
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: 60/073,629
;  PRIOR FILING DATE: 1998-04-02
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-09-730-893-4

  Query Match            100.0%;  Score 6;  DB 10;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 13
US-09-728-574-19
; Sequence 19, Application US/09728574
; Patent No. US20020137036A1
; GENERAL INFORMATION:
;  APPLICANT: Stratagene
;  TITLE OF INVENTION: Methods for Detection of a Target Nucleic Acid By Capture
;  FILE REFERENCE: 25436/1660
;  CURRENT APPLICATION NUMBER: US/09/728,574
;  CURRENT FILING DATE:  2000-11-30
;  PRIOR APPLICATION NUMBER: US 09/728574
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Drosophila sp.
;   FEATURE:
;   NAME/KEY: bicoid DNA binding site
;   LOCATION: (1)..(9)
US-09-728-574-19

  Query Match            100.0%;  Score 6;  DB 10;  Length 9;
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  Best Local Similarity   100.0%;  Pred. No. 2.5e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 6
US-09-817-387-29/c
; Sequence 29, Application US/09817387
; Patent No. US20010039263A1
; GENERAL INFORMATION:
;  APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin
;  TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof
;  FILE REFERENCE: 101195-24
;  CURRENT APPLICATION NUMBER: US/09/817,387
;  CURRENT FILING DATE:  2001-03-26
;  PRIOR APPLICATION NUMBER: DE 197 20 151.2
;  PRIOR FILING DATE: 1997-05-02
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  telomeric
;   OTHER INFORMATION: DNA of man
US-09-817-387-29

  Query Match             100.0%;  Score 6;  DB 10;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 7
US-09-735-363A-49/c
; Sequence 49, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
;  APPLICANT: Filion, Mario
;  APPLICANT:  Phillip, Nigel
;  TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
;  FILE REFERENCE: 02811-0181
;  CURRENT APPLICATION NUMBER: US/09/735,363A
;  CURRENT FILING DATE:  2000-12-12
;  PRIOR APPLICATION NUMBER: 60/170,325
;  PRIOR FILING DATE: 1999-12-13
;  PRIOR APPLICATION NUMBER: 60/228,925
;  PRIOR FILING DATE: 2000-08-29
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 49
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-49

  Query Match             100.0%;  Score 6;  DB 10;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 8
US-09-730-893-1/c
; Sequence 1, Application US/09730893
; Patent No. US20020107258A1
; GENERAL INFORMATION:
;  APPLICANT: KERWIN, SEAN M.
;  APPLICANT:  FEDOROFF, OLEG Y.
;  APPLICANT:  SALAZAR, MIGUEL
;  APPLICANT:  HURLEY, LAURENCE H.
;  TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
;  TITLE OF INVENTION:  G-QUADRUPLEX-INTERACTION COMPOUND
;  FILE REFERENCE: UTSB:679USC1
;  CURRENT APPLICATION NUMBER: US/09/730,893
;  CURRENT FILING DATE:  2000-12-05
;  PRIOR APPLICATION NUMBER: 09/244,675
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: 60/073,629
;  PRIOR FILING DATE: 1998-04-02
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-09-730-893-1

  Query Match             100.0%;  Score 6;  DB 10;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 9
US-09-940-173A-6/c
; Sequence 6, Application US/09940173A
; Publication No. US20030040525A1
; GENERAL INFORMATION:
;  APPLICANT: KERWIN, SEAN M.
;  APPLICANT:  FEDOROFF, OLEG Y.
;  APPLICANT:  SALAZAR, MIGUEL
;  APPLICANT:  HURLEY, LAURENCE H.
;  TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
;  TITLE OF INVENTION:  G-QUADRUPLEX-INTERACTION COMPOUND
;  FILE REFERENCE: UTSB:679USD2
;  CURRENT APPLICATION NUMBER: US/09/940,173A
;  CURRENT FILING DATE:  2002-06-24
;  PRIOR APPLICATION NUMBER: 09/730,893
;  PRIOR FILING DATE: 2000-12-05
;  PRIOR APPLICATION NUMBER: 09/244,675
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: 60/073,629
;  PRIOR FILING DATE: 1998-04-02
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-09-940-173A-6

  Query Match             100.0%;  Score 6;  DB 9;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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RESULT 2
US-10-122-630-12
; Sequence 12, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-018
;  CURRENT APPLICATION NUMBER: US/10/122,630
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 08/467,012
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US96/08386
;  PRIOR FILING DATE: 1996-06-03
;  PRIOR APPLICATION NUMBER: US 09/048,927
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-12

  Query Match             100.0%;  Score 6;  DB 9;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          1 CCCTAA 6


RESULT 3
US-10-122-633-11/c
; Sequence 11, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-11

  Query Match             100.0%;  Score 6;  DB 9;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
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Db          6 CCCTAA 1


RESULT 4
US-10-122-633-12
; Sequence 12, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-12

  Query Match             100.0%;  Score 6;  DB 9;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          1 CCCTAA 6


RESULT 5
US-09-940-173A-1/c
; Sequence 1, Application US/09940173A
; Publication No. US20030040525A1
; GENERAL INFORMATION:
;  APPLICANT: KERWIN, SEAN M.
;  APPLICANT:  FEDOROFF, OLEG Y.
;  APPLICANT:  SALAZAR, MIGUEL
;  APPLICANT:  HURLEY, LAURENCE H.
;  TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
;  TITLE OF INVENTION:  G-QUADRUPLEX-INTERACTION COMPOUND
;  FILE REFERENCE: UTSB:679USD2
;  CURRENT APPLICATION NUMBER: US/09/940,173A
;  CURRENT FILING DATE:  2002-06-24
;  PRIOR APPLICATION NUMBER: 09/730,893
;  PRIOR FILING DATE: 2000-12-05
;  PRIOR APPLICATION NUMBER: 09/244,675
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: 60/073,629
;  PRIOR FILING DATE: 1998-04-02
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-09-940-173A-1

  Query Match             100.0%;  Score 6;  DB 9;  Length 6;
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 08:30:00 ; Search time 65.5714 Seconds
(without alignments)
142.836 Million cell updates/sec

Title: US-09-540-843-12
Perfect score: 6
Sequence: 1 ccctaa 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 816406

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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c 3	6	100.0	6	9	US-10-122-633-11	Sequence 11, Appl
4	6	100.0	6	9	US-10-122-633-12	Sequence 12, Appl
c 5	6	100.0	6	9	US-09-940-173A-1	Sequence 1, Appli
c 6	6	100.0	6	10	US-09-817-387-29	Sequence 29, Appl
c 7	6	100.0	6	10	US-09-735-363A-49	Sequence 49, Appl
c 8	6	100.0	6	10	US-09-730-893-1	Sequence 1, Appli
c 9	6	100.0	7	9	US-09-940-173A-6	Sequence 6, Appli
c 10	6	100.0	7	10	US-09-730-893-6	Sequence 6, Appli
c 11	6	100.0	8	9	US-09-940-173A-4	Sequence 4, Appli
c 12	6	100.0	8	10	US-09-730-893-4	Sequence 4, Appli
13	6	100.0	9	10	US-09-728-574-19	Sequence 19, Appl
c 14	6	100.0	10	9	US-10-044-692-294	Sequence 294, App
c 15	6	100.0	10	9	US-10-044-539-294	Sequence 294, App
c 16	6	100.0	10	12	US-10-033-145-56	Sequence 56, Appl
c 17	6	100.0	10	12	US-10-033-145-358	Sequence 358, App
c 18	6	100.0	10	12	US-10-033-145-613	Sequence 613, App
c 19	6	100.0	10	12	US-10-033-145-1694	Sequence 1694, Ap
c 20	6	100.0	11	9	US-09-835-370-63	Sequence 63, Appl
c 21	6	100.0	11	9	US-10-122-630-5	Sequence 5, Appli
22	6	100.0	11	9	US-10-122-630-9	Sequence 9, Appli
c 23	6	100.0	11	9	US-10-122-633-5	Sequence 5, Appli
24	6	100.0	11	9	US-10-122-633-9	Sequence 9, Appli
25	6	100.0	11	9	US-09-249-155-57	Sequence 57, Appl
26	6	100.0	11	9	US-09-942-310-7	Sequence 7, Appli
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28	6	100.0	11	9	US-10-038-335-9	Sequence 9, Appli
29	6	100.0	11	10	US-09-057-351-2	Sequence 2, Appli
30	6	100.0	12	8	US-08-463-404-2	Sequence 2, Appli
c 31	6	100.0	12	8	US-08-463-404-3	Sequence 3, Appli
32	6	100.0	12	8	US-08-463-404-7	Sequence 7, Appli
33	6	100.0	12	9	US-10-132-002-1	Sequence 1, Appli
c 34	6	100.0	12	9	US-10-132-002-3	Sequence 3, Appli
35	6	100.0	12	9	US-10-073-118-18	Sequence 18, Appl
c 36	6	100.0	12	9	US-10-117-108A-41	Sequence 41, Appl
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c 38	6	100.0	12	9	US-09-984-664-11	Sequence 11, Appl
c 39	6	100.0	12	10	US-09-057-351-39	Sequence 39, Appl
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c 41	6	100.0	12	10	US-09-375-924C-6	Sequence 6, Appli
c 42	6	100.0	13	9	US-09-893-252-4	Sequence 4, Appli
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c 44	6	100.0	13	9	US-10-038-335-2	Sequence 2, Appli
c 45	6	100.0	14	8	US-08-591-486B-123	Sequence 123, App

ALIGNMENTS

RESULT 1
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; Sequence 11, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-11

Query Match 100.0%; Score 6; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          6 CCCTAA 1
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 07:52:05 ; Search time 31.0714 Seconds
(without alignments)
59.220 Million cell updates/sec

Title: US-09-540-843-12
Perfect score: 6
Sequence: 1 ccctaa 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 558892

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	6	100.0	6	1	US-08-381-097A-5	Sequence 5, Appli
	3	6	100.0	6	1	US-08-153-051B-4	Sequence 4, Appli
c	4	6	100.0	6	1	US-08-337-684-2	Sequence 2, Appli
	5	6	100.0	6	2	US-08-151-477A-4	Sequence 4, Appli
c	6	6	100.0	6	2	US-08-670-999-3	Sequence 3, Appli
c	7	6	100.0	6	3	US-08-729-598-4	Sequence 4, Appli
c	8	6	100.0	6	3	US-08-819-867-9	Sequence 9, Appli
	9	6	100.0	6	3	US-08-819-867-27	Sequence 27, Appl
c	10	6	100.0	6	3	US-08-630-019A-1	Sequence 1, Appli
c	11	6	100.0	6	3	US-09-018-545-3	Sequence 3, Appli
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c	14	6	100.0	7	3	US-08-729-598-8	Sequence 8, Appli
c	15	6	100.0	8	3	US-08-838-545-15	Sequence 15, Appl
	16	6	100.0	8	3	US-08-838-545-30	Sequence 30, Appl
c	17	6	100.0	8	3	US-08-838-545-34	Sequence 34, Appl
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	19	6	100.0	8	4	US-09-349-532-30	Sequence 30, Appl
c	20	6	100.0	8	4	US-09-349-532-34	Sequence 34, Appl
c	21	6	100.0	9	1	US-08-337-684-3	Sequence 3, Appli
c	22	6	100.0	9	3	US-08-630-019A-27	Sequence 27, Appl
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c	24	6	100.0	9	3	US-08-838-545-16	Sequence 16, Appl
c	25	6	100.0	9	4	US-09-349-532-16	Sequence 16, Appl
c	26	6	100.0	10	1	US-08-192-300-18	Sequence 18, Appl
c	27	6	100.0	10	2	US-08-531-743-10	Sequence 10, Appl
c	28	6	100.0	10	3	US-08-630-019A-8	Sequence 8, Appli
c	29	6	100.0	10	3	US-08-838-545-7	Sequence 7, Appli
	30	6	100.0	10	3	US-08-838-545-11	Sequence 11, Appl
c	31	6	100.0	10	3	US-08-838-545-17	Sequence 17, Appl
c	32	6	100.0	10	3	US-08-838-545-21	Sequence 21, Appl
	33	6	100.0	10	3	US-08-838-545-29	Sequence 29, Appl
c	34	6	100.0	10	4	US-08-974-549A-527	Sequence 527, App
c	35	6	100.0	10	4	US-09-349-532-7	Sequence 7, Appli
	36	6	100.0	10	4	US-09-349-532-11	Sequence 11, Appl
c	37	6	100.0	10	4	US-09-349-532-17	Sequence 17, Appl
c	38	6	100.0	10	4	US-09-349-532-21	Sequence 21, Appl
	39	6	100.0	10	4	US-09-349-532-29	Sequence 29, Appl
	40	6	100.0	11	1	US-08-330-123A-2	Sequence 2, Appli
	41	6	100.0	11	1	US-08-482-115B-2	Sequence 2, Appli
	42	6	100.0	11	2	US-08-660-678A-2	Sequence 2, Appli
c	43	6	100.0	11	2	US-08-531-743-11	Sequence 11, Appl
	44	6	100.0	11	2	US-08-531-743-12	Sequence 12, Appl
	45	6	100.0	11	2	US-08-485-778-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08-381-097A-3/c
; Sequence 3, Application US/08381097A
; Patent No. 5643890
; GENERAL INFORMATION:
; APPLICANT: Iverson, Patrick L.
; APPLICANT: Mata, John E.
; TITLE OF INVENTION: Synthteic Oligodeoxyribonucleotides
; TITLE OF INVENTION: Which Mimic Telomeric Sequences for Use in the Treatment
; TITLE OF INVENTION: of Cancer and Other Diseases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zarely, McKee, Thomte, Voorhees, & Sease
; STREET: 801 Grand Suite 3200
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: United States
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,097A
; FILING DATE: 31-JAN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: NEbel, Heidi S
; REGISTRATION NUMBER: 37,719
; REFERENCE/DOCKET NUMBER: unmc 63092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 515-288-3667
; TELEFAX: 515-288-1338
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-381-097A-3

Query Match 100.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          6 CCCTAA 1


RESULT 2
US-08-381-097A-5
; Sequence 5, Application US/08381097A
; Patent No. 5643890
;  GENERAL INFORMATION:
;    APPLICANT:  Iverson, Patrick L.
;    APPLICANT:  Mata, John E.
;    TITLE OF INVENTION:  Synthteic Oligodeoxyribonucleotides
;    TITLE OF INVENTION:  Which Mimic Telomeric Sequences for Use in the Treatment
;    TITLE OF INVENTION:  of Cancer and Other Diseases
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Zarely, McKee, Thomte, Voorhees, & Sease
;      STREET:  801 Grand Suite 3200
;      CITY:  Des Moines
;      STATE:  Iowa
;      COUNTRY:  United States
;      ZIP:  50309
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/381,097A
;      FILING DATE:  31-JAN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  NEbel, Heidi S
;      REGISTRATION NUMBER:  37,719
;      REFERENCE/DOCKET NUMBER:  unmc 63092
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  515-288-3667
;      TELEFAX:  515-288-1338
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-381-097A-5

  Query Match             100.0%;  Score 6;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          1 CCCTAA 6


RESULT 3
US-08-153-051B-4
; Sequence 4, Application US/08153051B
; Patent No. 5645986
;  GENERAL INFORMATION:
;    APPLICANT:  Michael D. West
;    APPLICANT:  Jerry W. Shay
;    APPLICANT:  Woodring E. Wright
;    APPLICANT:  Elizabeth Blackburn
;    APPLICANT:  Nam Woo Kim
;    APPLICANT:  Calvin B. Harley
;    APPLICANT:  Scott L. Weinrich
;    APPLICANT:  Catherine Strahl
;    APPLICANT:  Michael J. McEachern
;    APPLICANT:  Homayoun Vaziri
;    TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF
;    TITLE OF INVENTION:  CONDITIONS RELATED TO TELEOMERE
;    TITLE OF INVENTION:  LENGTH AND/OR TELOMERASE ACTIVITY
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/153,051B
;      FILING DATE:  No. 5645986ember 12, 1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/038,766
;      FILING DATE:  March 24, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  204/195
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-153-051B-4

  Query Match             100.0%;  Score 6;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          1 CCCTAA 6


RESULT 4
US-08-337-684-2/c
; Sequence 2, Application US/08337684
; Patent No. 5686306
;  GENERAL INFORMATION:
;    APPLICANT:  West, Michael David
;    APPLICANT:  Shay, Jerry
;    APPLICANT:  Wright, Woodring E.
;    TITLE OF INVENTION:  METHODS AND REAGENTS FOR
;    TITLE OF INVENTION:  MEASURING TELOMERES
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
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;       SOFTWARE:  Word Perfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/337,684
;       FILING DATE:  No. 5686306ember 10, 1994
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/151,477
;       FILING DATE:  No. 5686306ember 12, 1993
;       APPLICATION NUMBER:  08/153,051
;       FILING DATE:  No. 5686306ember 12, 1993
;       APPLICATION NUMBER:  08/060,952
;       FILING DATE:  May 13, 1993
;       APPLICATION NUMBER:  08/038,766
;       FILING DATE:  March 24, 1993
;       APPLICATION NUMBER:  07/882,438
;       FILING DATE:  May 13, 1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warburg, Richard J.
;       REGISTRATION NUMBER:  32,327
;       REFERENCE/DOCKET NUMBER:  210/085
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  6 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-337-684-2

  Query Match             100.0%;  Score 6;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 5
US-08-151-477A-4
; Sequence 4, Application US/08151477A
; Patent No. 5830644
;  GENERAL INFORMATION:
;    APPLICANT:  Michael D. West
;    APPLICANT:  Jerry W. Shay
;    APPLICANT:  Woodring E. Wright
;    APPLICANT:  Elizabeth Blackburn
;    APPLICANT:  Nam Woo Kim
;    APPLICANT:  Calvin B. Harley
;    APPLICANT:  Scott L. Weinrich
;    APPLICANT:  Catherine Strahl
;    APPLICANT:  Michael J. McEachern
;    APPLICANT:  Homayoun Vaziri
;    TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF
;    TITLE OF INVENTION:  CONDITIONS RELATED TO TELEOMERE
;    TITLE OF INVENTION:  LENGTH AND/OR TELOMERASE ACTIVITY
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/151,477A
;      FILING DATE:  No. 5830644ember 12, 1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/038,766
;      FILING DATE:  March 24, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  202/189
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-151-477A-4

  Query Match             100.0%;  Score 6;  DB 2;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          1 CCCTAA 6


RESULT 6
US-08-670-999-3/c
; Sequence 3, Application US/08670999
; Patent No. 5849727
;  GENERAL INFORMATION:
;    APPLICANT:  Porter, Thomas R.
;    APPLICANT:  Iverson, Patrick L.
;    TITLE OF INVENTION:  Compositions and Methods for Altering
;    TITLE OF INVENTION:  the Biodistribution of Biological Agents
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Zarley, McKee, Thomte, Voorhees & Sease
;      STREET:  801 Grand Suite 3200
;      CITY:  Des Moines
;      STATE:  Iowa
;      COUNTRY:  United States
;      ZIP:  50309
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/670,999
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nebel, Heidi S.
;      REGISTRATION NUMBER:  37,719
;      REFERENCE/DOCKET NUMBER:  unmc 107A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  515-288-3667
;      TELEFAX:  515-288-1338
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
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;    ANTI-SENSE:  YES
US-08-670-999-3

  Query Match             100.0%;  Score 6;  DB 2;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 7
US-08-729-598-4/c
; Sequence 4, Application US/08729598
; Patent No. 6001657
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Charles C.
;    APPLICANT:  Brown II, Bernard A.
;    APPLICANT:  Roberts, John J.
;    APPLICANT:  Pelsue, Stephen A.
;    TITLE OF INVENTION:  Antibodies That Selectively Bind
;    TITLE OF INVENTION:  Quadruplex Nucleic Acids
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sorojini J. Biswas
;      STREET:  P.O. Box 37428
;      CITY:  Raleigh
;      STATE:  No. 6001657th Carolina
;      COUNTRY:  USA
;      ZIP:  27627
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/729,598
;      FILING DATE:  11-OCT-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Biswas, Sorojini J.
;      REGISTRATION NUMBER:  39,111
;      REFERENCE/DOCKET NUMBER:  5051-301A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919) 854-1400
;      TELEFAX:  (919) 854-1401
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA (genomic)
US-08-729-598-4

  Query Match             100.0%;  Score 6;  DB 3;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 8
US-08-819-867-9/c
; Sequence 9, Application US/08819867
; Patent No. 6007989
;  GENERAL INFORMATION:
;    APPLICANT:  Michael D. West
;    APPLICANT:  Calvin B. Harley
;    APPLICANT:  Scott L. Weinrich
;    APPLICANT:  Catherine M. Strahl
;    APPLICANT:  Michael J. Mceachern
;    APPLICANT:  Jerry Shay
;    APPLICANT:  Woodring E. Wright
;    APPLICANT:  Elizabeth H. Blackburn
;    APPLICANT:  Nam Woo Kim
;    APPLICANT:  Homayoun Vaziri
;    TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF
;    TITLE OF INVENTION:  CONDITIONS RELATED TO
;    TITLE OF INVENTION:  TEOLOMERE LENGTH AND/OR
;    TITLE OF INVENTION:  TELOMERASE ACTIVITY
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,867
;      FILING DATE:  March 14, 1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/153,051
;      FILING DATE:  No. 6007989ember 12, 1993
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Chambers, Daniel M.
;      REGISTRATION NUMBER:  34,561
;      REFERENCE/DOCKET NUMBER:  224/232
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-819-867-9

  Query Match             100.0%;  Score 6;  DB 3;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 9
US-08-819-867-27
; Sequence 27, Application US/08819867
; Patent No. 6007989
;  GENERAL INFORMATION:
;    APPLICANT:  Michael D. West
;    APPLICANT:  Calvin B. Harley
;    APPLICANT:  Scott L. Weinrich
;    APPLICANT:  Catherine M. Strahl
;    APPLICANT:  Michael J. Mceachern
;    APPLICANT:  Jerry Shay
;    APPLICANT:  Woodring E. Wright
;    APPLICANT:  Elizabeth H. Blackburn
```

```
;    APPLICANT:  Nam Woo Kim
;    APPLICANT:  Homayoun Vaziri
;    TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF
;    TITLE OF INVENTION:  CONDITIONS RELATED TO
;    TITLE OF INVENTION:  TEOLOMERE LENGTH AND/OR
;    TITLE OF INVENTION:  TELOMERASE ACTIVITY
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,867
;      FILING DATE:  March 14, 1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/153,051
;      FILING DATE:  No. 6007989ember 12, 1993
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Chambers, Daniel M.
;      REGISTRATION NUMBER:  34,561
;      REFERENCE/DOCKET NUMBER:  224/232
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-819-867-27

  Query Match             100.0%;  Score 6;  DB 3;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          1 CCCTAA 6


RESULT 10
US-08-630-019A-1/c
; Sequence 1, Application US/08630019A
; Patent No. 6015710
;  GENERAL INFORMATION:
;    APPLICANT:  Shay, Jerry W.
;    APPLICANT:  Wright, Woodring E.
;    APPLICANT:  Piatyszek, Mieczyslaw A.
;    APPLICANT:  Corey, David
;    APPLICANT:  No. 6015710ton, James C.
;    TITLE OF INVENTION:  Modulation of Mammalian Telomerase by
;    TITLE OF INVENTION:  Peptide Nucleic Acids
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/630,019A
;      FILING DATE:  09-JUN-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-001600US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "peptide nucleic acid (PNA),
;      DESCRIPTION:  where (deoxy)ribose-phosphate linkages are replaced by
;      DESCRIPTION:  N-(2-aminoethyl)glycine units linked to nucleotide bases via
;      DESCRIPTION:  glycine amino nitrogen through a methylenecarbonyl linker"
US-08-630-019A-1

  Query Match             100.0%;  Score 6;  DB 3;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 11
US-09-018-545-3/c
; Sequence 3, Application US/09018545
; Patent No. 6087493
;  GENERAL INFORMATION:
;    APPLICANT:  Wheelhouse, Richard T.
;    APPLICANT:  Hurley, Laurence H.
;    TITLE OF INVENTION:  PORPHYRIN COMPOUNDS AS TELOMERASE
;    TITLE OF INVENTION:  INHIBITORS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/018,545
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/037,295
;      FILING DATE:  05-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  UTSB:654
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-018-545-3

  Query Match           100.0%;  Score 6;  DB 3;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 12
US-09-114-399-3/c
; Sequence 3, Application US/09114399
; Patent No. 6245747
; GENERAL INFORMATION:
;  APPLICANT:  Porter, Thomas R.
;  APPLICANT:  Iversen, Patrick L.
;  APPLICANT:  Meyer, Gary D.
;  TITLE OF INVENTION:  Targeted Site Specific Drug Delivery
;  TITLE OF INVENTION:  Compositions and Method of Use
;  FILE REFERENCE:  0450-0310.31
;  CURRENT APPLICATION NUMBER: US/09/114,399
;  CURRENT FILING DATE:  1998-07-13
;  PRIOR APPLICATION NUMBER:  US 08/615,495
;  PRIOR FILING DATE:  1996-03-12
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PS-ODN
US-09-114-399-3

  Query Match           100.0%;  Score 6;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 13
PCT-US96-01206-1/c
; Sequence 1, Application PC/TUS9601206
;  GENERAL INFORMATION:
;    APPLICANT:  Iverson, Patrick L.
;    APPLICANT:  Mata, John E.
;    TITLE OF INVENTION:  Synthetic Oligodeoxynucleotides Which
;    TITLE OF INVENTION:  Mimic Telomeric Sequences for Use in the Treatment of
;    TITLE OF INVENTION:  Cancer and other Diseases
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Zarley, McKee, Thomte, Voorhees & Sease
;      STREET:  801 Grand Avenue Suite 3200
;      CITY:  Des Moines
;      STATE:  Iowa
;      COUNTRY:  United States
;      ZIP:  50309
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/01206
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/381,097
;      FILING DATE:  31-JAN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  NEbel, Heidi S.
;      REGISTRATION NUMBER:  37,719
;      REFERENCE/DOCKET NUMBER:  UNMC# 63092
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  515-288-3667
;      TELEFAX:  515-288-1338
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
PCT-US96-01206-1

  Query Match           100.0%;  Score 6;  DB 5;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          6 CCCTAA 1


RESULT 14
US-08-729-598-8/c
; Sequence 8, Application US/08729598
; Patent No. 6001657
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Charles C.
;    APPLICANT:  Brown II, Bernard A.
;    APPLICANT:  Roberts, John J.
;    APPLICANT:  Pelsue, Stephen A.
;    TITLE OF INVENTION:  Antibodies That Selectively Bind
;    TITLE OF INVENTION:  Quadruplex Nucleic Acids
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sorojini J. Biswas
;      STREET:  P.O. Box 37428
;      CITY:  Raleigh
;      STATE:  No. 6001657th Carolina
;      COUNTRY:  USA
;      ZIP:  27627
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/729,598
;      FILING DATE:  11-OCT-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Biswas, Sorojini J.
;      REGISTRATION NUMBER:  39,111
;      REFERENCE/DOCKET NUMBER:  5051-301A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919) 854-1400
;      TELEFAX:  (919) 854-1401
;  INFORMATION FOR SEQ ID NO:  8:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA (genomic)
US-08-729-598-8

  Query Match             100.0%;  Score 6;  DB 3;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          7 CCCTAA 2


RESULT 15
US-08-838-545-15/c
; Sequence 15, Application US/08838545
; Patent No. 6046307
;  GENERAL INFORMATION:
;    APPLICANT:  Shay, Jerry W.
;    APPLICANT:  Wright, Woodring E.
;    APPLICANT:  Piatyszek, Mieczyslaw A.
;    APPLICANT:  Corey, David R.
;    APPLICANT:  No. 6046307ton, James C.
;    TITLE OF INVENTION:  Modulation of Mammalian Telomerase by
;    TITLE OF INVENTION:  Peptide Nucleic Acids
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/838,545
;      FILING DATE:  09-APR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,019
;      FILING DATE:  09-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-001610US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "peptide nucleic acid (PNA),
;      DESCRIPTION:  where (deoxy(ribose-phosphate linkages are replaced by
;      DESCRIPTION:  N-(2-aminoethyl)glycine units linked to nucleotide bases via
;      DESCRIPTION:  glycine amino N through a methylenecarbonyl linker"
US-08-838-545-15

  Query Match             100.0%;  Score 6;  DB 3;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCTAA 6
              ||||||
Db          7 CCCTAA 2


Search completed:  July  6, 2003, 09:42:21
Job time :  32.0714 secs
```